



FA

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07H 21/04, C07K 5/00, A61K 38/00, 35/12	A1	(11) International Publication Number: WO 98/21228 (43) International Publication Date: 22 May 1998 (22.05.98)
(21) International Application Number: PCT/US97/21821 (22) International Filing Date: 13 November 1997 (13.11.97) (30) Priority Data: 08/751,517 15 November 1996 (15.11.96) US 08/801,092 14 February 1997 (14.02.97) US (71) Applicant: CANJI, INC. [US/US]; 3030 Science Park Road, San Diego, CA 92121 (US). (72) Inventors: ANTELMAN, Douglas; 1716 Swallowtail Road, Encinitas, CA 92024 (US). GREGORY, Richard, J.; 2 Wintergreen Lane, Westford, MA 01886 (US). WILLS, Kenneth, N.; 821 Bluffcrest Lane, Encinitas, CA 92024 (US). (74) Agents: FITTS, Renee, A. et al.; Townsend and Townsend and Crew LLP, 8th floor, Two Embarcadero Center, San Francisco, CA 94111-3834 (US).	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: TISSUE SPECIFIC EXPRESSION OF RETINOBLASTOMA PROTEIN (57) Abstract Fusions of the transcription factor E2F and the retinoblastoma protein RB are provided, along with methods of treatment of hyperproliferative diseases.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

5 **TISSUE SPECIFIC EXPRESSION OF RETINOBLASTOMA**
PROTEIN

BACKGROUND OF THE INVENTION

10 Both the retinoblastoma gene (RB) and transcription
factor E2F play a critical role in cell growth control (for a
review, see Adams, P. & Kaelin, W. Seminars in Cancer Biology
6:99-108 (1995)). The RB locus is frequently inactivated in a
variety of human tumor cells. Reintroduction of a wild-type
15 RB gene (e.g., Bookstein et al. Science 247:712-715 (1990)) or
RB protein (pRB) (e.g., Antelman et al. Oncogene 10:697-
704(1995)) into RBneg/RBmut cells can suppress growth in
culture and tumorigenicity in vivo.

20 While E2F serves to activate transcription of S-
phase genes, its activity is kept in check by RB. RB arrests
cells by blocking exit from G into S-phase (for example, Dowdy
et al. Cell 73:499-511 (1993)) but the precise pathway of the
arrest remains unclear.

25 Although E2F forms complexes with RB, complex
formation is more efficient if an E2F-related protein, DP-1,
is present. E2F-1 and DP-1 form stable heterodimers which
bind to DNA (for example, Qin et al. Genes and Dev. 6-:953-964
(1992)). DP-1-E2F complexes serve to cooperatively activate
transcription of E2F-dependent genes. Such transcription can
30 be repressed by pRB in the same manner as E2F-1 or DP-1
activated transcription.

35 Transcriptional repression of genes by RB in some
instances can be achieved by tethering pRB to a promoter. For
example, GAL4-pRB fusions bind to GAL4 DNA binding domains and
repress transcription from p53, Sp-1 or AP-1 elements (Adnane,
et al. J. Biol. Chem. 270:8837-8843 (1995); Weintraub, et al.
Nature 358:259-261 (1995)). Sellers, et al. (Proc. Natl.
Acad. Sci. 92:11544-11548 (1995)) disclosed fusions of amino

acid residues 1-368 of E2F with amino acids 379-792 or 379-928 of RB.

Chang, et al. (Science 267:518-521 (1995)) disclosed the use of a replication-defective adenovirus-RB construct in the reduction of neointima formation in two animal models of restenosis, a hyperproliferative disorders.

SUMMARY OF THE INVENTION

The instant invention provides the surprising result that a fusion of an E2F polypeptide with an RB polypeptide is more efficient in repressing transcription of the E2F promoter than RB alone, and that such fusions can cause cell cycle arrest in a variety of cell types. Such fusions can thus address the urgent need for therapy of hyperproliferative disorders, including cancer.

One aspect of the invention is a polypeptide comprising a fusion of a transcription factor, the transcription factor comprising a DNA binding domain, and a retinoblastoma (RB) polypeptide, the RB polypeptide comprising a growth suppression domain. Another aspect of the invention is DNA encoding such a fusion polypeptide. The DNA can be inserted in an adenovirus vector.

In some embodiments of the invention, the transcription factor is E2F. The cyclin A binding domain of the E2F can be deleted or nonfunctional. The E2F can comprise amino acid residues about 95 to about 194 or about 95 to about 286 in some embodiments.

The retinoblastoma polypeptide can be wild-type RB, RB56, or a variant or fragment thereof. In some embodiments, the retinoblastoma polypeptide comprises amino acid residues of about 379 to about 928. Preferred amino acid substitutions of the RB polypeptide include residues 2, 608, 788, 807, and 811.

Another aspect of the invention is an expression vector comprising DNA encoding a polypeptide, the polypeptide comprising a fusion of a transcription factor, the transcription factor comprising a DNA binding domain, and a retinoblastoma (RB) polypeptide, the RB polypeptide comprising

a growth suppression domain. In some embodiments a tissue-specific promoter is operatively linked to DNA encoding the fusion polypeptide. The tissue-specific promoter can be a smooth muscle alpha actin promoter.

5 Another aspect of the invention is a method for treatment of hyperproliferative disorders comprising administering to a patient a therapeutically effective dose of an E2F-RB fusion polypeptide. The hyperproliferative disorder can be cancer. In some embodiments the hyperproliferative
10 disorder is restenosis. The fusion polypeptide and nucleic acid encoding the fusion polypeptide can be used to coat devices used for angioplasty.

BRIEF DESCRIPTION OF THE DRAWINGS

15 Figure 1A depicts the predicted amino acid sequence of E2F.

Figure 1B depicts the nucleotide sequence of transcription factor E2F.

Figure 2A depicts the nucleotide sequence of pRB as
20 disclosed by Lee, et al. (Nature 329:642-645 (1987)).

Figure 2B depicts the predicted amino acid sequence of pRB.

Figure 3 is a diagrammatic representation of pCTM.

Figure 4 depicts the nucleotide sequence of plasmid
25 pCTM.

Figure 5 is a diagrammatic representation of pCTMI.

Figure 6 depicts the nucleotide sequence of pCTMI.

Figure 7 is a diagrammatic representation of plasmid
pCTMIE.

30 Figure 8 depicts the nucleotide sequence of pCTMIE.

Figure 9 is a diagram depicting E2F-RB fusion constructs used in the examples. All E2F constructs commenced at amino acid 95 and lacked part of the cyclin A binding domain. E2F-437 contained the DNA binding domain (black),
35 heterodimerization domain (white), and the transactivation domain (stippled). E2F-194 contained solely the DNA binding domain. E2F-286 contained the DNA binding domain and the DP-1 heterodimerization domain. To generate E2F-194-RB56-5s and

E2F-286-RB56-5s, the E2F constructs were fused in-frame to codon 379 of RB. C706F is an inactivating point mutation.

Figure 10 is a diagram depicting transcriptional repression by E2F-RB fusion constructs.

5 Figure 11 (A-D) depicts expression of E2F-RB fusion proteins in mammalian cell lines. Extracts were prepared from cells used in E2-CAT reporter assays or in FACS assays and analyzed with an anti-RB monoclonal antibody. In panel A, the results are shown from C33A cells transfected with (3) RB56-H209, (4) RB56 wild-type, (5) RB56-5s, (6) E2F286-5s, (7)
10 E2F194-5s, (8) E2F194, (9) E2F286, (10) E2F437. Lane (1) is an RB56 protein standard. Lane (2) is a mock transfection. In panel B, results are shown for transfection of Saos-2 cells with (1) RB56, (2,3) E2F194-5s, and (4,5) E2F286-5s. In panel
15 C, results are shown for transfection of 5637 cells with (2,3) RB56 wild-type, (4,5) RB56-5s; (6,7) E2F194-5s; (7,8) E2F286-5s. Lane (1) is an RB56 protein standard. In panel D, results are shown for NIH-3T3 transfected (3) RB56, (4)
20 E2F286-5s, (5) E2F194-5s. Lane (1) is an RB56 standard; lane (2) is an RB110 standard.

Figure 12 depicts histogram analyses of flow cytometry of RB-expressing NIH-3T3 cells.

Figure 13, panel A, depicts a comparison of the effects of a CMV-driven recombinant adenovirus (ACN56) with
25 two isolates of a human smooth muscle alpha actin-driven E2F-p56 fusion construct consisting of amino acids 95 through 286 of E2F linked directly and in-frame to p56 (amino acids 379-928 of RB cDNA), vs. a control virus (ACN) in a ³H-thymidine uptake assay in the rat smooth muscle cell line A7R5. Panel
30 (B) depicts the effects of the same constructs in the rat smooth muscle cell line A10.

Figure 14 depicts a comparison of the effects of the viruses described in Fig. 13 in non-muscle cells. Panel (A) depicts results in the breast carcinoma cell line MDA MB468.
35 Panel (B) depicts results in the non-small cell lung cell carcinoma line H358.

Figure 15, top panel, depicts the relative infectivity by adenovirus of different cell lines as judged by

the level of β -galactosidase (β -gal) staining following infection with equal amounts of a recombinant adenovirus expressing β -gal driven by a CMV promoter. H358 is non-small lung cell carcinoma cell line; MB468 is a breast carcinoma cell line; A7R5 and A10 are smooth muscle cell lines. The lower portion of the figure depicts the relative levels of p56 protein expressed in the same cells when infected with the recombinant adenovirus ACN56, in which the p56 cDNA is driven by the non-tissue specific CMV promoter.

Figure 16 depicts relative protein levels in cells infected with the smooth muscle alpha actin promoter-driven E2F-p56 fusion construct (ASN286-56). UN denoted uninfected; 50, 100, 250, and 500 refer to multiplicities of infection (MOI).

Figure 17 is a bar graph depicting the ratio of intima to media area (as a measurement of the inhibition of neointima formation) from cross-sections (n=9) of rat carotid arteries which were injured and treated with recombinant adenoviruses expressing either β -gal, RB (ACNRB) or p56 (ACN56), all under the control of the CMV promoter.

Figure 18 is a series of three photographs depicting restenosis in a rat angioplasty model. The panel on the left depicts data from a normal animal; the central panel depicts data from an animal injured and then treated with a β -gal expressing recombinant virus; the panel on the right depicts data from an animal injured and then treated with a recombinant adenovirus expressing p56 (ACN56).

Figure 19 depicts tissue-specificity of the smooth muscle alpha actin promoter, as demonstrated by its selective ability to express the β -gal transgene in muscle cells but not non-muscle cells. The panels on the left compare β -gal expression in the breast cell carcinoma line MB468 infected with either an MOI=1 with a CMV-driven β -gal (ACNBGAL) vs an MOI= 100 with the smooth muscle promoter construct (ASNBGAL). The panels on the right show β -gal expression of the rat smooth muscle cell line A7R5 infected with either an MOI=1 of ACNBGAL or an MOI=50 of ASNBGAL. Expression from ASNBGAL is seen in the muscle cell line, but is absent in the non-muscle

cell line, despite the higher degree of infectivity of the cells.

Figure 20 depicts the ability of recombinant adenovirus expressing RB to transduce rat carotid arteries. recombinant adenovirus-treated arteries (1×10^9 pfu) were harvested two days following balloon injury and infection. Cross sections were fixed and an RB specific antibody was used to detect the presence of RB protein in the tissue. The control virus used was ACN. RB protein staining was evident in the ACNRB treated sample, especially at higher magnifications.

Figure 21 depicts a comparison of the effects of a CMV-driven p56 recombinant adenovirus (ACN56E4) vs a human smooth muscle alpha-actin promoter-driven E2F-p56 fusion construct (ASN286-56) vs control adenoviral constructs containing either the CMV or smooth muscle alpha-actin promoters without a downstream transgene (ACNE3 or ASBE3-2 isolates shown, respectively). Assays were ^3H -thymidine uptake either in a smooth muscle cell line (A7R5) or a non-muscle cell line (MDA-MB468, breast carcinoma). Results demonstrated muscle tissue specificity using the smooth muscle alpha-actin promoter and specific inhibition by both the p56 and E2F-p56 transgenes relative to their respective controls.

DESCRIPTION OF THE PREFERRED EMBODIMENT

The instant invention provides RB fusion constructs including fusion polypeptides and vectors encoding them, and methods for the use of such constructs in the treatment of hyperproliferative diseases. In some preferred embodiments of the invention, an RB polypeptide is fused to an E2F polypeptide. Any E2F species can be used, typically E2F-1, -2, -3, -3, or -5 (see, e.g., Wu et al. Mol. Cell. Biol. 15:2536-2546 (1995); Ivey-Hoyle et al. Mol. Cell. Biol. 13:7802 (1993); Vairo et al. Genes and Dev. 9:869 (1995); Beijersbergen et al. Genes and Dev. 8:2680 (1994)); Ginsberg et al. Genes and Dev. 8:2665 (1994); Buck et al. Oncogene 11:31 (1995)), more typically E2F-1. Typically, the EF2

polypeptide comprises at least the DNA binding domain of E2F, and may optionally include the cyclin A binding domain, the heterodimerization domain, and/or the transactivation domain. Preferably, the cyclin A binding domain is not functional.

5 The nucleotide and amino acid sequence of E2F referred to herein are those of Genbank HUME2F, shown in Figure 1A and 1B. Nucleic acid, preferably DNA, encoding such an EF2 polypeptide is fused in reading frame to an RB polypeptide. The RB
10 polypeptide can be any RB polypeptide, including conservative amino acid variants, allelic variants, amino acid substitution, deletion, or insertion mutants, or fragments thereof. Preferably, the growth suppression domain, i.e., amino acids residues 379-928, of the RB polypeptide is functional (Hiebert, et al. MCB 13:3384-3391 (1993); Qin, et
15 al. Genes and Dev. 6:953-964 (1992)). In some embodiments, wild-type pRB110 is used. More preferably, a truncated version of RB, RB56, is used. RB56 comprises amino acid residues 379-928 of pRB110 (Hiebert, et al. MCB 13:3384-3391 (1993); Qin, et al. Genes and Dev. 6:953-964 (1992)). In some
20 embodiments, amino acid variants of RB at positions 2, 608, 612, 788, 807, or 811, are used singly or in combination. The variant RB56-5s comprises wild-type RB56 having alanine substitutions at 608, 612, 788, 807, and 811. Numbering of RB amino acids and nucleotides is according to the RB sequence
25 disclosed by Lee, et al. (Nature 329:642-645 (1987)), hereby incorporated by reference in its entirety for all purposes. (Figure 2).

Nucleic acids encoding the polypeptides of the invention can be DNA or RNA. The phrase "nucleic acid
30 sequence encoding" refers to a nucleic acid which directs the expression of a specific protein or peptide. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein. The nucleic acid sequences include both the
35 full length nucleic acid sequences as well as non-full length sequences derived from the full length protein. It is further understood that the sequence includes the degenerate codons of

the native sequence or sequences which may be introduced to provide codon preference in a specific host cell.

The term "vector" as used herein refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids. Where a recombinant microorganism or cell culture is described as hosting an "expression vector," this includes both extrachromosomal circular DNA and DNA that has been incorporated into the host chromosome(s). Where a vector is being maintained by a host cell, the vector may either be stably replicated by the cells during mitosis as an autonomous structure, or is incorporated within the host's genome. A vector contains multiple genetic elements positionally and sequentially oriented, i.e., operatively linked with other necessary elements such that nucleic acid in the vector encoding the constructs of the invention can be transcribed, and when necessary, translated in transfected cells.

The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, and termination regions. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

The term "plasmid" refers to an autonomous circular DNA molecule capable of replication in a cell, and includes both the expression and nonexpression types. Where a recombinant microorganism or cell culture is described as hosting an "expression plasmid", this includes both extrachromosomal circular DNA molecules and DNA that has been incorporated into the host chromosome(s). Where a plasmid is being maintained by a host cell, the plasmid is either being stably replicated by the cells during mitosis as an autonomous structure or is incorporated within the host's genome.

The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

In general, a construct of the invention is provided in an expression vector comprising the following elements linked sequentially at appropriate distances for functional expression: a tissue-specific promoter, an initiation site for transcription, a 3' untranslated region, a 5' mRNA leader sequence, a nucleic acid sequence encoding a polypeptide of the invention, and a polyadenylation signal. Such linkage is termed "operatively linked." Enhancer sequences and other sequences aiding expression and/or secretion can also be included in the expression vector. Additional genes, such as those encoding drug resistance, can be included to allow selection or screening for the presence of the recombinant vector. Such additional genes can include, for example, genes encoding neomycin resistance, multi-drug resistance, thymidine kinase, beta-galactosidase, dihydrofolate reductase (DHFR), and chloramphenicol acetyl transferase.

In the instant invention, tissue-specific expression of the RB constructs of the invention is preferably accomplished by the use of a promoter preferentially used by a tissue of interest. Examples of tissue-specific promoters include the promoter for creatine kinase, which has been used to direct the expression of dystrophin cDNA expression in muscle and cardiac tissue (Cox, et al. Nature 364:725-729 (1993)) and immunoglobulin heavy or light chain promoters for the expression of suicide genes in B cells (Maxwell, et al. Cancer Res. 51:4299-4304 (1991)). An endothelial cell-specific regulatory region has also been characterized (Jahroudi, et al. Mol. Cell. Biol. 14:999-1008 (1994)).

Amphotrophic retroviral vectors have been constructed carrying a herpes simplex virus thymidine kinase gene under the control of either the albumin or alpha-fetoprotein promoters (Huber, et al. Proc. Natl. Acad. Sci. U.S.A. 88:8039-8043 (1991)) to target cells of liver lineage and hepatoma cells, respectively. Such tissue specific promoters can be used in retroviral vectors (Hartzoglou, et al. J. Biol. Chem. 265:17285-17293 (1990)) and adenovirus vectors (Friedman, et al. Mol. Cell. Biol. 6:3791-3797 (1986); Wills et al. Cancer Gene Therapy 3:191-197 (1995)) and still retain their tissue specificity.

In the instant invention, a preferred promoter for tissue-specific expression of exogenous genes is the human smooth muscle alpha-actin promoter. Reddy, et al. (J. Cell Biology 265:1683-1687 (1990)) disclosed the isolation and nucleotide sequence of this promoter, while Nakano, et al. (Gene 99:285-289 (1991)) disclosed transcriptional regulatory elements in the 5' upstream and the first intron regions of the human smooth muscle (aortic type) alpha-actin gene.

Petropoulos, et al. (J. Virol. 66:3391-3397 (1992)) disclosed a comparison of expression of bacterial chloramphenicol transferase (CAT) operatively linked to either the chicken skeletal muscle alpha actin promoter or the cytoplasmic beta-actin promoter. These constructs were provided in a retroviral vector and used to infect chicken eggs.

Exemplary tissue-specific expression elements for the liver include but are not limited to HMG-CoA reductase promoter (Luskey, Mol. Cell. Biol. 7(5):1881-1893 (1987)); sterol regulatory element 1 (SRE-1; Smith et al. J. Biol. Chem. 265(4):2306-2310 (1990); phosphoenol pyruvate carboxy kinase (PEPCK) promoter (Eisenberger et al. Mol. Cell Biol. 12(3):1396-1403 (1992)); human C-reactive protein (CRP) promoter (Li et al. J. Biol. Chem. 265(7):4136-4142 (1990)); human glucokinase promoter (Tanizawa et al. Mol. Endocrinology 6(7):1070-81 (1992); cholesterol 7-alpha hydroylase (CYP-7) promoter (Lee et al. J. Biol. Chem. 269(20):14681-9 (1994)); beta-galactosidase alpha-2,6 sialyltransferase promoter

(Svensson et al. J. Biol. Chem. 265(34):20863-8 (1990); insulin-like growth factor binding protein (IGFBP-1) promoter (Babajko et al. Biochem Biophys. Res. Comm. 196 (1):480-6 (1993)); aldolase B promoter (Bingle et al. Biochem J. 294(Pt2):473-9 (1993)); human transferrin promoter (Mendelzon et al. Nucl. Acids Res. 18(19):5717-21 (1990); collagen type I promoter (Houglum et al. J. Clin. Invest. 94(2):808-14 (1994)).

Exemplary tissue-specific expression elements for the prostate include but are not limited to the prostatic acid phosphatase (PAP) promoter (Banas et al. Biochim. Biophys. Acta 1217(2):188-94 (1994); prostatic secretory protein of 94 (PSP 94) promoter (Nolet et al. Biochim. Biophys. ACTA 1098(2):247-9 (1991)); prostate specific antigen complex promoter (Casper et al. J. Steroid Biochem. Mol. Biol. 47 (1-6):127-35 (1993)); human glandular kallikrein gene promoter (hgt-1) (Lilja et al. World J. Urology 11(4):188-91 (1993)).

Exemplary tissue-specific expression elements for gastric tissue include but are not limited to the human H⁺/K⁺-ATPase alpha subunit promoter (Tanura et al. FEBS Letters 298:(2-3):137-41 (1992)).

Exemplary tissue-specific expression elements for the pancreas include but are not limited to pancreatitis associated protein promoter (PAP) (Dusetti et al. J. Biol. Chem. 268(19):14470-5 (1993)); elastase 1 transcriptional enhancer (Kruse et al. Genes and Development 7(5):774-86 (1993)); pancreas specific amylase and elastase enhancer promoter (Wu et al. Mol. Cell. Biol. 11(9):4423-30 (1991); Keller et al. Genes & Dev. 4(8):1316-21 (1990)); pancreatic cholesterol esterase gene promoter (Fontaine et al. Biochemistry 30(28):7008-14 (1991)).

Exemplary tissue-specific expression elements for the endometrium include but are not limited to the uteroglobin promoter (Helftenbein et al. Annal. NY Acad. Sci. 622:69-79 (1991)).

Exemplary tissue-specific expression elements for adrenal cells include but are not limited to cholesterol side-

chain cleavage (SCC) promoter (Rice et al. J. Biol. Chem. 265:11713-20 (1990)).

Exemplary tissue-specific expression elements for the general nervous system include but are not limited to gamma-gamma enolase (neuron-specific enolase, NSE) promoter (Forss-Petter et al. Neuron 5(2):187-97 (1990)).

Exemplary tissue-specific expression elements for the brain include but are not limited to the neurofilament heavy chain (NF-H) promoter (Schwartz et al. J. Biol. Chem. 269(18):13444-50 (1994)).

Exemplary tissue-specific expression elements for lymphocytes include but are not limited to the human CGL-1/granzyme B promoter (Hanson et al. J. Biol. Chem. 266(36):24433-8 (1991)); the terminal deoxy transferase (TdT), lambda 5, VpreB, and lck (lymphocyte specific tyrosine protein kinase p56lck) promoter (Lo et al. Mol. Cell. Biol. 11(10):5229-43 (1991)); the humans CD2 promoter and its 3'transcriptional enhancer (Lake et al. EMBO J. 9(10):3129-36 (1990)), and the human NK and T cell specific activation (NKG5) promoter (Houchins et al. Immunogenetics 37(2):102-7 (1993)).

Exemplary tissue-specific expression elements for the colon include but are not limited to pp60c-src tyrosine kinase promoter (Talamonti et al. J. Clin. Invest 91(1):53-60 (1993)); organ-specific neoantigens (OSNs), mw 40kDa (p40) promoter (Ilantzis et al. Microbiol. Immunol. 37(2):119-28 (1993)); colon specific antigen-P promoter (Sharkey et al. Cancer 73(3 supp.) 864-77 (1994)).

Exemplary tissue-specific expression elements for breast cells include but are not limited to the human alpha-lactalbumin promoter (Thean et al. British J. Cancer. 61(5):773-5 (1990)).

Other elements aiding specificity of expression in a tissue of interest can include secretion leader sequences, enhancers, nuclear localization signals, endosmolytic peptides, etc. Preferably, these elements are derived from the tissue of interest to aid specificity.

Techniques for nucleic acid manipulation of the nucleic acid sequences of the invention such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labelling probes, DNA hybridization, and the like are described generally in Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al."

Once DNA encoding a sequence of interest is isolated and cloned, one can express the encoded proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

The E2F-RB fusion constructs of the invention can be introduced into the tissue of interest in vivo or ex vivo by a variety of methods. In some embodiments of the invention, the nucleic acid, preferably DNA, is introduced to cells by such methods as microinjection, calcium phosphate precipitation, liposome fusion, or biolistics. In further embodiments, the DNA is taken up directly by the tissue of interest. In other embodiments, the constructs are packaged into a viral vector system to facilitate introduction into cells.

Viral vector systems useful in the practice of the instant invention include adenovirus, herpesvirus, adeno-associated virus, minute virus of mice (MVM), HIV, sindbis virus, and retroviruses such as Rous sarcoma virus, and MoMLV. Typically, the constructs of the instant invention are inserted into such vectors to allow packaging of the E2F-RB expression construct, typically with accompanying viral DNA, infection of a sensitive host cell, and expression of the E2F-RB gene. A particularly advantageous vector is the adenovirus vector disclosed in Wills, et al. Human Gene Therapy 5:1079-1088 (1994).

In still other embodiments of the invention, the recombinant DNA constructs of the invention are conjugated to a cell receptor ligand for facilitated uptake (e.g., invagination of coated pits and internalization of the endosome) through a DNA linking moiety (Wu, et al. J. Biol. Chem. 263:14621-14624 (1988); WO 92/06180). For example, the DNA constructs of the invention can be linked through a polylysine moiety to asialo-oromucoid, which is a ligand for the asialoglycoprotein receptor of hepatocytes.

Similarly, viral envelopes used for packaging the constructs of the invention can be modified by the addition of receptor ligands or antibodies specific for a receptor to permit receptor-mediated endocytosis into specific cells (e.g., WO 93/20221, WO 93/14188; WO 94/06923). In some embodiments of the invention, the DNA constructs of the invention are linked to viral proteins, such as adenovirus particles, to facilitate endocytosis (Curiel, et al. Proc. Natl. Acad. Sci. U.S.A. 88:8850-8854 (1991)). In other

embodiments, molecular conjugates of the instant invention can include microtubule inhibitors (WO 94/06922); synthetic peptides mimicking influenza virus hemagglutinin (Plank, et al. J. Biol. Chem. 269:12918-12924 (1994)); and nuclear
5 localization signals such as SV40 T antigen (WO 93/19768).

In some embodiments of the invention, the RB polypeptides of the invention are administered directly to a patient in need of treatment. A "therapeutically effective" dose is a dose of polypeptide sufficient to prevent or reduce
10 severity of a hyperproliferative disorder. As used herein, the term "hyperproliferative cells" includes but is not limited to cells having the capacity for autonomous growth, i.e., existing and reproducing independently of normal regulatory mechanisms. Hyperproliferative diseases may be
15 categorized as pathologic, i.e., deviating from normal cells, characterizing for constituting disease, or may be categorized as non-pathologic, i.e., deviation from normal but not associated with a disease state. Pathologic hyperproliferative cells are characteristic of the following
20 disease states: restenosis, diabetic retinopathy, thyroid hyperplasia, Grave's disease, psoriasis, benign prostatic hypertrophy, Li-Fraumeni syndrome including breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer, various leukemias and lymphomas. Examples of
25 non-pathological hyperproliferative cells are found, for instance, in mammary ductal epithelial cells during development of lactation and also in cells associated with wound repair. Pathological hyperproliferative cells characteristically exhibit loss of contact inhibition and a
30 decline in their ability to selectively adhere which implies a further breakdown in intercellular communication. These changes include stimulation to divide and the ability to secrete proteolytic enzymes.

The constructs of the invention are useful in the
35 therapy of various cancers and other conditions in which the administration of RB is advantageous, including but not limited to peripheral vascular diseases and diabetic retinopathy. Although any tissue can be targeted for which

some tissue-specific expression element, such as a promoter, can be identified, of particular interest is the tissue-specific administration of an RB construct for hyperproliferative disorders such as restenosis, for which the smooth muscle actin promoter is preferable.

The compositions of the invention will be formulated for administration by manners known in the art acceptable for administration to a mammalian subject, preferably a human. In some embodiments of the invention, the compositions of the invention can be administered directly into a tissue by injection or into a blood vessel supplying the tissue of interest. In further embodiments of the invention the compositions of the invention are administered "locoregionally", i.e., intravesically, intralesionally, and/or topically. In other embodiments of the invention, the compositions of the invention are administered systemically by injection, inhalation, suppository, transdermal delivery, etc. In further embodiments of the invention, the compositions are administered through catheters or other devices to allow access to a remote tissue of interest, such as an internal organ. The compositions of the invention can also be administered in depot type devices, implants, or encapsulated formulations to allow slow or sustained release of the compositions.

The invention provides compositions for administration which comprise a solution of the compositions of the invention dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents,

wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

The concentration of the compositions of the invention in the pharmaceutical formulations can vary widely, i.e., from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of administration selected.

The compositions of the invention may also be administered via liposomes. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations the composition of the invention to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a desired target, such as antibody, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired composition of the invention of the invention can delivered systemically, or can be directed to a tissue of interest, where the liposomes then deliver the selected therapeutic/immunogenic peptide compositions.

Liposomes for use in the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, e.g., liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, e.g., Szoka et al. Ann. Rev. Biophys. Bioeng. 9:467 (1980), U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369, incorporated herein by reference.

A liposome suspension containing a composition of the invention may be administered intravenously, locally, topically, etc. in a dose which varies according to, inter alia, the manner of administration, the composition of the

invention being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example,
5 pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally
10 employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more compositions of the invention of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the compositions of the
15 invention are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of compositions of the invention are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant.
20 Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters,
25 such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, e.g., lecithin for intranasal
30 delivery.

The constructs of the invention can additionally be delivered in a depot-type system, an encapsulated form, or an implant by techniques well-known in the art. Similarly, the constructs can be delivered via a pump to a tissue of
35 interest.

In some embodiments of the invention, the compositions of the invention are administered ex vivo to cells or tissues explanted from a patient, then returned to

the patient. Examples of ex vivo administration of gene therapy constructs include Arteaga et al. Cancer Research 56(5):1098-1103 (1996); Nolta et al. Proc Natl. Acad. Sci. USA 93(6):2414-9 (1996); Koc et al. Seminars in Oncology 23 (1):46-65 (1996); Raper et al. Annals of Surgery 223(2):116-26 (1996); Dalesandro et al. J. Thorac. Cardi. Surg. 11(2):416-22 (1996); and Makarov et al. Proc. Natl. Acad. Sci. USA 93(1):402-6 (1996).

In some embodiments of the invention, the constructs of the invention are administered to a cardiac artery after balloon angioplasty to prevent or reduce the severity of restenosis. The constructs of the invention can be used to coat the device used for angioplasty (see, for example, Willart, et al. Circulation 89:2190-2197 (1994); French, et al. Circulation 90:2402-2413 (1995)). In further embodiments, the fusion polypeptides of the invention can be used in the same manner.

The following examples are included for illustrative purposes and should not be considered to limit the present invention.

EXAMPLES

Example I

E2F-RB Fusions

A. Introduction

In this example, expression plasmids which encode different segments of E2F fused to RB56 polypeptide were constructed. RB56 is a subfragment of full length RB which contains the "pocket" domains necessary for growth suppression (Hiebert, et al. MCB 13:3384-3391 (1993); Qin, et al. Genes and Dev. 6:953-964 (1992)). E2F194 contains E2F amino acids 95-194. This fragment contains only the DNA binding domain of E2F. E2F286 contains the DNA binding domain and the DP-1 heterodimerization domain. Both E2F fragments lack the N-terminal cyclin A-kinase binding domain, which appears to down-regulate the DNA binding activity of E2F (Krek et al. Cell 83:1149-1158 (1995); Krek et al. Cell 78:161-172 (1994)).

B. Construction of Vectors

Plasmid pCTM contains a CMV promoter, a tripartite adenovirus leader flanked by T7 and SP6 promoters, and a multiple cloning site with a bovine growth hormone (BGH) polyadenylation site and a SV-40 poly adenylation site downstream. A diagrammatic representation of pCTM is provided in Figure 3. The DNA sequence for pCTM is provided in Figure 4.

pCTMI was constructed from pCTM by digesting pCTM with Xho I and Not I and subcloning a 180 bp intron XhoI-Not I fragment from a pCMV- β -gal vector (Clonetech). A diagrammatic representation of pCTMI is provided in Figure 5. The DNA sequence is provided in Figure 6.

pCTMIE was constructed by amplifying the SV40 enhancer from SV40 viral DNA in a polymerase chain reaction. The amplified product was digested with BglII and inserted into BamHI-digested pCMTI and ligated in the presence of BamHI. The plasmid is depicted diagrammatically in Figure 7. The DNA sequence is provided in Figure 8.

pCTM-RB was prepared as follows. A 3.2 KB Xba I - Cla I fragment of pETRBc (Huang et al. Nature 350:160-162 (1991)) containing the full length human RB cDNA was ligated to Xba I-Cla I digested pCTM. pCTM-RB56 was prepared by ligating the digested pCTM to a 1.7 KB Xba I -Cla I fragment containing the coding sequence for RB56. pCTMI-RB, pCTMIE-RB, pCTMI-RB56(amino acids 381-928) and pCTMIE-RB56(amino acids 381-928) were all constructed by the same methods.

C. RB-E2F fusion Constructs

Figure 9 depicts the fusion constructs used in these studies. These E2F constructs commenced at amino acid 95 and lacked part of the cyclin A binding domain. E2F437 contained the DNA binding domain (black), heterodimerization domain (white) and transactivation domain (stippled). E2F194 contained solely the DNA binding domain. E2F286 contained the DNA binding domain and DP-1 heterodimerization domain. RB56-5s refers to an RB variant having alanine substitutions at amino acid residues 606, 612, 788, 807 and 811. In E2F194-

RB56-5s and E2F286-RB56-5s, the E2F fragments were fused in frame to codon 379 of RB-5s. RB56-C706F contained an inactivating point mutation (Kaye et al. Proc. Natl. Acad. Sci. U.S.A. 87:6922-6926 (1990)).

5 pCMV-E2F194 and pCMV-E2F437 were constructed as follows. DNA encoding amino acids 95-194 of E2F (containing the DNA binding domain) or amino acids 95-437 was amplified in a polymerase chain reaction, digested with HindII, and ligated into SmaI/HindII digested pCMV-RB56 vectors. pCMVE2F286 was
10 constructed by digesting pCMV-E2F437 with AflIII, treating the ends with DNA pol I (Klenow fragment) and religating in the presence of AflIII. The blunt end ligation created a stop codon at position 287. pCMV-E2F286-5s was constructed by ligating AflIII (blunt)/HindIII digested pE2F437 to a Sal I
15 (blunt)-HindIII fragment containing the RB56-5s coding sequence. pCTMIE-E2F194-5s and pCTMIE-E2F286-RB5s were constructed by ligating EcoRI-EcoRV digested pCTMIE (4.2 KB) to HindIII (blunt)-EcoRI fragments from either pCMV-E2F194-RB5s or pCMV-E2F286-RB5s.

20 D. Promoter Repression

To measure the effect of the E2F-RB fusion proteins, cervical carcinoma cell line C33A (ATCC # HTB-31) was transfected with equivalent amounts of E2F194-RB56 or E2F RB56
25 with an E2-CAT reporter plasmid (See, e.g., Weintraub et al. Nature 358:259-261 (1992)).

In the C33A assay, 250,000 C33A cells were seeded into each of well of 6-well tissue culture plates and allowed to adhere overnight. 5 μ g each of pCMV-RB56, pCMV-E2F RB56,
30 or pCMV-E2F plasmid were cotransfected (calcium phosphate method, MBS transfection kit, Stratagene) with 5 μ g of indicated reporter construct E2-CAT or SVCAT) and 2.5 μ g β -gal plasmid (pCMV- β , Clontech) per well into duplicate wells. Cells were harvested 72 hour after transfection and extracts
35 were prepared.

In the 5637 assay, 250,000 5637 cells were seeded as described above. 1 μ g each of RB or E2F-RB fusion plasmid, E2-CAT or SV-CAT reporter plasmid and pCMV- β -galactosidase

were cotransfected using the lipofectin reagent (BRL, Bethesda, Maryland) according to the manufacturer's instructions.

CAT assays were performed using either 20 μ L (C33A) or 50 μ L (5637) of cell extract (Gorman et al. Mol. Cell. Biol. 2:1044 (1982)). TLCs were analyzed on a Phosphorimager SF (Molecular Dynamics). CAT activities were normalized for transfection efficiency according to β -galactosidase activities of each extract. β -galactosidase activities of extracts were assayed as described by Rosenthal et al. (Meth. Enzym. 152:704 (1987)).

The results of these studies were as follows. Transfection of the E2-CAT reporter alone or in the presence of the nonfunctional control RB56-H209 mutant yielded relatively high CAT activity. Cotransfection of wild-type RB56 or the variant RB56-5s resulted in a 10 to 12 fold repression of CAT activity, indicating that RB56 or RB56-5s are both capable of efficiently repressing E2F-dependent transcription. E2F194-RB5s and E2F286-RB5s repressed transcription approximately 50 fold. Transcriptional repression required both the RB56 and the E2F components of the fusion proteins, as expression of E2F194 and E2F286 did not mediate transcriptional repression. No repression of SV40-CAT transcription occurred with E2F-RB constructs, thus demonstrating the specificity of the transcriptional repression by E2FRB for the E2 promoter. These results are depicted diagrammatically in Figure 10.

E. Cell cycle arrest

The ability of E2F-RB fusion polypeptides to cause G1 arrest in Saos-2 (RB-/- cells) (ATCC # HTB-85) and C33A cells was investigated. Previous studies have shown that RB-mediated E2 promoter repression and G1 arrest are linked in Saos-2 cells but dissociated in C33A (RBmut) cells (Xu, et al. PNAS 92:1357-1361 (1992)). Cells were washed in PBS and were fixed in 1 mL -20°C 70% ethanol for 30 minutes. Cells were collected by centrifugation and resuspended in 0.5 mL 2% serum containing 10 μ g/ml RNase A and incubated for 30 minutes at

37°C 0.5 mL of PBS containing propidium iodide (100 µg/ml) was added to each sample, mixed and cells were filtered through a FACS tube capstrainer. FACS analysis was performed on a FACS-Scan (Becton-Dickenson) using doublet discrimination. 5,000-10,000 CD20+ events were analyzed. Percent of cells in G₀/G₁, S, and G₂/M was determined using Modfit modeling software.

The results of this experiment were as follows.

Both full length RB110 and the truncated version RB56, but not the control mutant RB-H209, caused G₁ arrest in Saos-2 cells (Table 1). Similarly, the RB56-5s, E2F-194-RB56-5s and E2F286-RB56-5s all were capable of arresting cells in G₀/G₁. Transfection of the DNA binding domain, E2F194, did not block S-phase entry in Saos-2 as previously described for rodent cells (Dobrowolski, et al. *Oncogene* 9:2605-2612 (1994)). In contrast, RB110, RB56, and E2F-RB fusion proteins were not capable of arresting C33A cell lines indicating that the transcriptional repression observed in these cells does not translate into G₁ arrest.

The ability of the E2F-RB fusion proteins to arrest 5637 cells was also investigated (Table 2). RB56 and RB56-5s both efficiently arrested cells in G₀/G₁ (approximately 90% of cells in G₀-G₁), whereas E2F194-RB56-5s and E2F286-RB56-5s are slightly less efficient (about 80% of cells in G₀/G₁) at promoting G₀/G₁ arrest. Without being limited to any one theory, the less efficient arrest of both Saos-2 and 5637 cells by the E2F-RB fusion proteins appears due to the lower levels of steady-state protein produced in these cells (Figure 11, panels b and c).

Table 1: Cell Cycle Regulation by RB and E2F-RB fusion proteins in RBneg cells

% Cells			
	CD20 ⁺ G ₀ /G ₁	G ₂ /M	S-phase
H209	52.1	27.1	20.8
p56RB	78.8	14.2	7.0
p110RB	70.9	14.3	14.8

p56RB-5s	84.8	13.2	2.0
p56RB-p5	81.3	11.5	7.3
E2F-194-5s	77.8	14.9	7.3
E2F-286-5s	72.2	15.0	12.8
E2F-194	49.9	28.0	22.1

Table 2: Growth Suppression of 5637 Bladder Cells by RB and E2F-RB fusion proteins

5637/CD20 ⁺	% Cells		
	G ₀ /G ₁	S	G ₂ M
CD20	59.7	16.9	20.6
RB56-C706F	57.4	16.3	24.3
RB56WT	90.7	4.12	4.88
RB56-5s	89.91	3.51	6.1
E2F1 94-5s	80.1	1.31	0
E2F-286-5s	79.21	8.1	0

F. Activity of Fusion Proteins in Functional RB Background

The activity of the E2F-RB fusion proteins in a cellular background containing functional RB was then determined. NIH-3T3 cells were transfected with RB56 or E2F-RB56 fusions and stained with anti-RB monoclonal antibody 3C8 (Wen et al. *J. Immuno. Meth.* 169:231-240 (1994)). FACS analysis was performed of the RB expressing cells. The results are shown in Figure 12. The non-gated population (g) shows the characteristic cell cycle distribution for NIH-3T3 cells (60% G₀, 28% S, 10% G₂/M). In contrast, in cells transfected with RB56 (a,b) or E2F-RB fusion proteins (c-f), greater than 90% of the RB-expressing cells were arrested in G₀, G₁. These data demonstrate that the ability of RB and E2F-RB56 fusions to arrest cells in G₀/G₁ is not limited to RB negative tumor cells. The relative levels of protein expressed in transfected NIH-3T3 cells was also investigated. RB110 was not expressed efficiently in these cells.

Thus, these data demonstrate that E2F-RB fusion proteins are more efficient transcriptional repressors than either pRB or RB56 alone, and that RB can repress transcription by remaining bound to E2F rather than directly blocking the transactivation domain of E2F. These data support the use of E2F-RB fusions as RB agonists in both RB+ cells and in RB negative or RB mutant cells.

Example II.

Tissue-Specific Expression of E2F-RB Fusions

A. Construction of Recombinant Adenovirus:

In this experiment, recombinant adenoviruses comprising an RB polypeptide under the control of a CMV or smooth muscle alpha actin promoter were generated.

The smooth muscle α -actin promoter (bases -670 through +5, Reddy et al. "Structure of the Human Smooth Muscle α -Actin Gene." J. Biol. Chem. 265:1683-1687 (1990), Nakano, et al. "Transcriptional Regulatory Elements In The 5' Upstream and First Intron Regions of The Human Smooth Muscle (aortic type) α -Actin-Encoding Gene." Gene 99:285-289 (1991) was isolated by PCR from a genomic library with 5' Xho I and Avr II and 3' Xba I, Cla I and Hind III restriction sites added for cloning purposes. The fragment was subcloned as an Xho I, Hind III fragment into a plasmid for sequencing to verify base composition. A fusion construct 286-56 containing the DNA and heterodimerization domain of E2F-1 (bases 95-286) linked to p56 (amino acids 379-928 of full length RB) was subcloned as an Xba I, Cla I fragment directly downstream of the smooth muscle α -actin promoter, and this expression cassette was digested out and cloned into the plasmid pAd/ITR/IX- as an Xba I to AvrII, and Cla I fragment to create the plasmid pASN286-56. This plasmid consisted of the adenovirus type 5 inverted terminal repeat (ITR), packaging signals and Ela enhancer, followed by the human smooth muscle α -actin promoter and 286-56 cassette, and then Ad 2 sequence 4021-10462 (which contains the Elb/protein IX poly A signal) in a pBR322 background. Recombinant adenovirus was produced by standard procedures.

The plasmid pASN286-56 was linearized with Ngo MI and co-transfected into 293 cells with the large fragment of Cla I digested rAd34 which has deletions in both the E3 and E4 regions of adenovirus type 5. Ad34 was a serotype 5 derivative with a 1.9 KB deletion in early region 3 resulting from deletion of the Xba I restriction fragment extending from Ad5 coordinates 28593 to 30470 and a 1.4 KB deletion of early region 4 resulting from a Taq I fragment of E4 (coordinates 33055-35573) being replaced with a cDNA containing E4 ORF 6 and 6/7.

Recombinant adenovirus produced by homologous recombination was isolated and identified by restriction digest analysis and further purified by limiting dilution. Additional control recombinant adenoviruses are described elsewhere and include the control virus ACN (CMV promoter, Wills, et al. "Gene Therapy For Hepatocellular Carcinoma: Chemosensitivity Conferred By Adenovirus-Mediated Transfer of The HSV-1 Thymidine Kinase Gene." Cancer Gene Therapy 2:191-197 (1995)), and ACN56 (RB expressed under control of a CMV promoter).

ACN56 was prepared as follows. A plasmid containing p56 cDNA was constructed by replacing the p53 cDNA from the plasmid ACNP53 (Wills et al. Human Gene Therapy 5:1079-1088 (1994)) with a 1.7 KB Xba I- BamHI fragment isolated from plasmid pET 9a-Rb56 (Antelman et al. Oncogene 10:697-704 (1995)) which contains p56 cDNA. The resulting plasmid contained amino acids 381-928 of p56, the Ad5 inverted terminal repeat, viral packaging signals and Ela enhancer, followed by the human cytomegalovirus immediate early promoter (CMV) and Ad 2 tripartite leader cDNA to drive p56 expression. The p56 cDNA was followed by Ad 2 sequence 4021-10462 in a pBR322 background. This plasmid was linearized with EcoRI and cotransfected with the large fragment of bsp 106 digested DL327 (E3 deleted; Thimmappaaya et al. Cell 31:543-551 (1982)) or h5ile4 (E4 deleted; Hemstrom et al. J. Virol. 62:3258-3264 (1988)). Recombinant viruses were further purified by limiting dilution.

B. Cellular Proliferation

In this experiment, cell lines were infected in culture with recombinant adenovirus RB constructs to ascertain the relative expression of the RB polypeptide and the effect on cell proliferation.

For H358 (ATCC # Crl 5807) and MDA-MB468 (ATCC # HTB 132, breast adenocarcinoma) cells, 5,000 cell/well were plated in normal growth media in a 96 well microtiter plate (Costar) and allowed to incubate overnight at 37°C, 7% CO₂. Viruses were serially diluted in growth media and used to infect cells at the indicated doses for 48 hours. At this point, ³H-thymidine was added (Amersham, 0.5 µCi/well) and the cells were incubated at 37°C for another 3 hours prior to harvest. Both A7r5 (ATCC CRL1444, rat smooth muscle) and A10 (ATCC CRL 1476, rat smooth muscle) cells were seeded at 3,000 cells/well in either DME + 0.5% FCS or DME + 20% FCS respectively. Virus was serially diluted in the seeding media and used to infect the cells at the doses indicated in the Figures. The infection and labelling procedure were the same for A10 cells as with the H358 and MDA-MB468 cells except that 2 µCi/well of label was used. The A7r5 cells were not infected with virus until 48 hours after seeding. Forty eight hours after infection, the serum concentration was raised to 10% FCS and 2 µCi/well of ³H-thymidine was added and incubation continued for an additional 3 hours prior to harvest. All cells were harvested by aspirating media from the wells, trypsinization of the cells, and harvesting using a 96 well GF/C filter with a Packard Top count cell harvester. Results are plotted as the mean percentage (+/- SD) of media treated control proliferation versus dose of virus in Figures 13 and 14.

Thus, Figure 13 depicts a comparison of the effects of adenovirus p56 constructs on muscle cells A10 and A7R5 cells. The CMV-driven p56 (ACN 56) virus inhibited A10 growth to approximately the same extent as the actin promoter-driven E2F-fusion constructs (ASN586-56 #25,26). In Figure 14, the effects of adenovirus constructs on inhibition of a breast cancer cell line, MDA Mβ468 and a non-small cell lung carcinoma cell line, H358, are depicted. In these

experiments, actin promoter-driven E2F-p56 was ineffective, while the CMV promoter-driven p56 was effective in inhibiting growth of non-smooth muscle cells.

To determine whether the non-smooth muscle cells were more infectable with adenovirus than the smooth muscle cell lines used, the four cell lines, H358, MB468, A7R5, and A10 were infected at an MOI of 5 with an adenovirus expressing β -galactosidase (AC β GL; Wills, et al. Human Gene Therapy 5:1079-1088 (1994)) and degree of β -gal staining was examined. As shown in Figure 15 (top), the non-smooth muscle cell lines were significantly more infectable than the smooth muscle cell lines. In a further test, cells were infected at higher multiplicities of infection (50, 100, 250, 500) with ACN56 and the amount of p56 present in the infected cells detected by autoradiography. As can be seen in Figure 15 (bottom), the non-muscle cell lines had significantly more p56 present, since as a result of their greater infectivity, infected cells have a greater viral load and thus more copies of the p56 template driven by the non-tissue specific CMV promoter.

In a further experiment, the specificity of the actin smooth muscle promoter for smooth muscle tissue was ascertained. In this experiment, β -gal expression levels in cells infected with β -gal constructs driven with different promoters were measured. As can be seen in Figure 19, despite the lower infectivity of the smooth muscle cells, expression was only evident in these cells using the smooth muscle alpha actin promoter.

Figure 21 depicts a comparison of the effects of a CMV driven p56 recombinant adenovirus (ACN56E4) vs a human smooth muscle alpha-actin promoter driven E2F-p56 fusion construct (ASN286-56) vs control adenoviral construct containing either the CMV or smooth muscle alpha-actin promoters without a downstream transgene (ACNE3 or ASBE3-2 isolates shown, respectively). Assays were 3H-thymidine uptake either in a smooth muscle cell line (A7R5) or a non-muscle cell line (MDA-MB468, breast carcinoma). Results demonstrated muscle tissue specificity using the smooth muscle

alpha-actin promoter and specific inhibition of both the p56 and E2F-p56 transgenes relative to their respective controls.

C. Inhibition of Restenosis

5 The model of balloon injury was based on that described by Clowes, et al. (Clowes, Lab. Invest. 49:327-333 (1983)). Male Sprague-Dawley rats weighing 400-500g were anesthetized with an intraperitoneal injection of sodium pentobarbital (45 mg/kg. Abbot Laboratories, North Chicago, Illinois). The bifurcation of the left common carotid artery was exposed through a midline incision and the left common, internal, and external carotid arteries were temporarily ligated. A 2F embolectomy catheter (Baxter Edwards Healthcare Corp., Irvine, CA) was introduced into the external carotid and advanced to the distal ligation of the common carotid. 10 The balloon was inflated with saline and drawn towards the arteriotomy site 3 times to produce a distending, deendothelializing injury. the catheter was then withdrawn. Adenovirus (1×10^9 pfu of Ad-RB (ACNRb) or Ad-p56 (ACN56) in a volume of $10\mu\text{l}$ diluted to $100\mu\text{l}$ with 15% (wt/vol) Poloxamer 20 407 (BASF, Parsippany, N.J.) or Ad- β -Gal (1×10^9 pfu, diluted as above) was injected via a canula, inserted just proximal to the carotid bifurcation into a temporarily isolated segment of the artery. The adenovirus solution was incubated for 20 25 minutes after which the viral infusion was withdrawn and the cannula removed. The proximal external carotid artery was then ligated and blood flow was restored to the common carotid artery by release of the ligatures. The experimental protocol was approved by the Institutional Animal Care and Use 30 Committee and complied with the "Guide for the Care and Use of Laboratory Animals." (NIH Publication No. 86-23, revised 1985).

 Rats were sacrificed at 14 days following treatment with an intraperitoneal injection of pentobarbital (100 35 mg/kg.). The initially balloon injured segment of the left common carotid artery, from the proximal edge of the omohyoid muscle to the carotid bifurcation, was perfused with saline and dissected free of the surrounding tissue. The tissue was

fixed in 100% methanol until imbedded in paraffin. Several 4-
µm sections were cut from each tissue specimen. One section
from each specimen was stained with hematoxylin and eosin and
another with Richardson's combination elastic-trichrome stain
5 conventional light microscopic analysis.

Histological images of cross sections of hematoxylin
and eosin or elastic-trichrome stained arterial sections were
projected onto a digitizing board (Summagraphics) and the
intimal, medial and luminal areas were measured by
10 quantitative morphometric analysis using a computerized
sketching program (MACMEASURE, version 1.9, National Institute
of Mental Health).

Results were expressed as the mean \pm S.E.M.
Differences between groups were analyzed using an unpaired
15 two-tailed Student's t test. Statistical significance was
assumed when the probability of a null effect was <0.05 .

Results are shown in Figures 17 and 18. In Figure
17, the relative inhibition of neointima formation is depicted
graphically, demonstrating the ability of p56 and RB to
20 inhibit neointima formation. Figure 18 provides photographic
evidence of the dramatic reduction of neointima in the
presence of p56.

Adenovirus-treated carotid arteries were harvested
from rats at 2 days following balloon injury and infections.
25 Tissue was fixed in phosphate-buffered formalin until embedded
in paraffin. Tissue was cut into 4µm cross-sections and
dewaxed through xylene and graded alcohols. Endogenous
peroxidase was quenched with 1% hydrogen peroxide for 30
minutes. Antigen retrieval was performed in 10mM sodium
30 citrate buffer, pH 6.0 at 95°C for 10 minutes. A monoclonal
anti-RB antibody (AB-5, Oncogene Sciences, Uniondale, New
York) was applied 10µg/ml in PBS in a humid chamber at 4°C for
24 hours. Secondary antibody was applied from the Unitect
Mouse Immunohistochemistry Kit (Oncogene Sciences, Uniondale,
35 New York) according to the manufacturer's instructions. The
antibody complexes were visualized using 3,3'-diaminobenzidine
(DAB, Vector Laboratories, Burlingame, CA). Slides were thin

counterstained with hematoxylin and mounted. The results are depicted in Figure 20.

5 All references cited herein are hereby incorporated
by reference in their entirety for all purposes.

WHAT IS CLAIMED IS:

- 1 1. A polypeptide comprising a fusion of a
2 transcription factor, the transcription factor comprising a
3 DNA binding domain, and a retinoblastoma (RB) polypeptide, the
4 RB polypeptide comprising a growth suppression domain.
- 1 2. A nucleic acid encoding the fusion polypeptide
2 of claim 1.
- 1 3. The nucleic acid of claim 2, wherein the
2 nucleic acid is inserted in an adenovirus vector.
- 1 4. The polypeptide of claim 1, wherein the
2 transcription factor is E2F.
- 1 5. The polypeptide of claim 4, wherein the cyclin
2 A binding domain of the E2F is deleted or nonfunctional.
- 1 6. The polypeptide of claim 1, wherein the
2 retinoblastoma polypeptide is RB56.
- 1 7. The polypeptide of claim 1, wherein the
2 retinoblastoma polypeptide is wild type RB.
- 1 8. The polypeptide of claim 1, wherein the
2 retinoblastoma polypeptide comprises from about amino acid
3 residue 379 to about amino acid residue 928 of pRB.
- 1 9. The polypeptide of claim 1, wherein the
2 retinoblastoma polypeptide comprises at least one substitution
3 of amino acid residues selected from the group consisting of
4 2, 608, 612, 788, 807, and 811 of pRB.
- 1 10. The polypeptide of claim 5, wherein the E2F
2 comprises about amino acid residues 95 to about 286.

1 11. The polypeptide of claim 4, wherein the E2F
comprises about amino acid residues 95 to about 194.

1 12. The polypeptide of claim 1, wherein the fusion
2 comprises EF2 amino acid residues from about 95 to about 194
3 operatively linked to RB amino acid residues from about 379 to
4 about 928.

1 13. An expression vector comprising DNA encoding a
2 polypeptide, the polypeptide comprising a fusion of a
3 transcription factor, the transcription factor comprising a
4 DNA binding domain, and a retinoblastoma (RB) polypeptide, the
5 RB polypeptide comprising a growth suppression domain.

1 14. The vector of claim 13, comprising a tissue-
2 specific promoter operatively linked to DNA encoding the
3 fusion.

1 15. The vector of claim 14, wherein the tissue
2 specific promoter is a smooth muscle actin promoter.

1 16. A method for treatment of a hyperproliferative
2 disorder in a patient comprising administering to a patient a
3 therapeutically effective dose of a fusion polypeptide
4 comprising a fusion of a transcription factor, the
5 transcription factor comprising a DNA binding domain, and a
6 retinoblastoma (RB) polypeptide, the RB polypeptide comprising
7 a growth suppression domain.

1 17. The method of claim 16, wherein the fusion
2 protein is encoded by a nucleic acid delivered to the patient.

1 18. The method of claim 16, wherein the
2 transcription factor is E2F.

1 19. The method of claim 18, wherein the cyclin A
2 binding domain of the E2F is deleted or nonfunctional.

1 20. The method of claim 16, wherein the RB is RB56.

1 21. The method of claim 16, wherein the RB is wild
2 type RB56.

1 22. The method of claim 16, wherein the RB
2 comprises from about amino acid residue 379 to about amino
3 acid residue 928.

1 23. The method of claim 16, wherein the RB
2 comprises at least one substitution of amino acid residues
3 selected from the group consisting of 2, 608, 612, 788, 807,
4 and 811.

1 24. The method of claim 18, wherein the E2F
2 comprises about amino acid residues 95 to about 286.

1 25. The method of claim 18, wherein the E2F
2 comprises about amino acid residues 95 to about 194.

1 26. The method of claim 16, wherein the fusion
2 comprises EF2 amino acid residues from about 95 to about 194
3 operatively linked to RB amino acid residues from about 379 to
4 about 928.

1 27. The method of claim 18, wherein the E2F -RB
2 fusion polypeptide is expressed under the control of a tissue-
3 specific promoter.

1 28. The method of claim 27, wherein the tissue
2 specific promoter is a smooth muscle actin promoter.

1 29. The method of claim 16, wherein the
2 hyperproliferative disorder is cancer.

1 30. The method of claim 29, wherein the cancer is
2 bladder cancer.

1 31. The method of claim 29, wherein the
2 hyperproliferative disorder is restenosis.

1 32. The method of claim 31, wherein the E2F-RB
2 fusion polypeptide is administered after angioplasty.

1 33. The method of claim 32, wherein the E2F-RB
2 fusion polypeptide is administered as a coating on an
3 angioplasty device.

1 34. The method of claim 17, wherein the nucleic
2 acid is administered after angioplasty.

1 35. The method of claim 17, wherein the nucleic
2 acid is administered as a coating on an angioplasty device.

1 36. The method of claim 17, wherein the nucleic
2 acid is inserted in an adenovirus vector.

1/51

10	20	30	40	50	60
MALAGAPAGG	PCAPALEALL	GAGALRL LDS	SQIVIISAAQ	DASAPPAPTG	PAAPAAGPCD
70	80	90	100	110	120
PDLLL FATPQ	APRPTPSAPR	PALGRPPVKR	RLDLETDH QY	LAESSGPARG	RGRHPGKGVK
130	140	150	160	170	180
SPGEKSRYET	SLNLTTKRFL	ELLSHSADGV	VDLNWAAEVL	KVQKRRIYDI	TNVLEGIQLI
190	200	210	220	230	240
AKKSKNHIQW	LGSHTTVGVG	GRLEGLTQDL	RQLQESEQQL	DHLMNICTTQ	LRLLSEDTDS
250	260	270	280	290	300
QRLAYVTCQD	LRSIADPAEQ	MVMVIKAPPE	TQLQAVDSSE	NFQISLKSKQ	GPIDVFLCPE
310	320	330	340	350	360
ETVGGISPGK	TPSQEVTSEE	ENRATDSATI	VSPPPSSPPS	SLTTDPSQSL	LSLEQEPLLS
370	380	390	400	410	420
RMGSLRAPVD	EDRLSPLVAA	DSLLEHVRED	FSGLLPEEFI	SLSPPEALD	YHFGLEE GEG
430	440	450	460	470	480
IRDLFDCDFG	DLTPLDF*...

FIG. 1A

2/51

10	20	30	40	50	60
GGAATTCCGT	GGCCGGGACT	TTGCAGGCAG	CGGCGGCCCG	GGGCGGAGCG	GGATCGAGCC
70	80	90	100	110	120
CTCGCCGAGG	CCTGCCGCCA	TGGGCCCCGCG	CCGCCGCCGC	CGCCTGTCAC	CCGGGCCGCG
130	140	150	160	170	180
CGGGCCGTGA	GCGTCATGGC	CTTGCCCGGG	GCCCCCTGCG	GCGGCCCATG	CGCGCCGGCG
190	200	210	220	230	240
CTGGAGGCC	TGCTCGGGGC	CGGCGCGCTG	CGGCTGCTCG	ACTCCTCGCA	GATCGTCATC
250	260	270	280	290	300
ATCTCCGCCG	CGCAGGACGC	CAGCGCCCCG	CCGGCTCCCA	CCGGCCCCGC	GGCGCCCCGC
310	320	330	340	350	360
GCCGGCCCCCT	GCGACCCTGA	CCTGCTGCTC	TTCGCCACAC	CGCAGGCGCC	CCGGCCCCACA
370	380	390	400	410	420
CCCAAGTGGC	CGCGGCCCGC	GCTCGGCCCG	CCGCCGGTGA	AGCGGAGGCT	GGACCTGGAA
430	440	450	460	470	480
ACTGACCATC	AGTACCTGGC	CGAGAGCAGT	GGGCCAGCTC	GGGGCAGAGG	CCGCCATCCA
490	500	510	520	530	540
GGAAAAGGTG	TGAAATCCCC	GGGGGAGAAG	TCACGCTATG	AGACCTCACT	GAATCTGACC
550	560	570	580	590	600
ACCAAGCGCT	TCCTGGAGCT	GCTGAGCCAC	TCGGCTGACG	GTGTCTGCGA	CCTGAACTGG
610	620	630	640	650	660
GCTGCCGAGG	TGCTGAAGGT	GCAGAAGCGG	CGCATCTATG	ACATCACCAA	CGTCCTTGAG
670	680	690	700	710	720
GGCATCCAGC	TCATTGCCAA	GAAGTCCAAG	AACCACATCC	AGTGGCTGGG	CAGCCACACC
730	740	750	760	770	780
ACAGTGGGCG	TCGGCGGACG	GCTTGAGGGG	TTGACCCAGG	ACCTCCGACA	GCTGCAGGAG
790	800	810	820	830	840
AGCGAGCAGC	AGCTGGACCA	CCTGATGAAT	ATCTGTACTA	CGCAGCTGCG	CCTGCTCTCC
850	860	870	880	890	900
GAGGACACTG	ACAGCCAGCG	CCTGGCCTAC	GTGACGTGTC	AGGACCTTCG	TAGCATTGCA
910	920	930	940	950	960
GACCCTGCAG	AGCAGATGGT	TATGGTGATC	AAAGCCCTC	CTGAGACCCA	GCTCCAAGCC
970	980	990	1000	1010	1020
GTGGACTCTT	CGGAGAACTT	TCAGATCTCC	CTTAAGAGCA	AACAAGGCC	GATCGATGTT
1030	1040	1050	1060	1070	1080
TTCTGTGCC	CTGAGGAGAC	CGTAGGTGGG	ATCAGCCCTG	GGAAGACCCC	ATCCAGGAG
1090	1100	1110	1120	1130	1140
GTCATTCTTG	AGGAGGAGAA	CAGGGCCACT	GACTCTGCCA	CCATAGTGTC	ACCACCACCA
1150	1160	1170	1180	1190	1200
TCATCTCCCC	CCTCATCCCT	CACCACAGAT	CCCAGCCAGT	CTCTACTCAG	CCTGGAGCAA
1210	1220	1230	1240	1250	1260
GAACCGCTGT	TGTCCCGGAT	GGGCAGCCTG	CGGGCTCCCG	TGGACGAGGA	CCGCCTGTCC

FIG. 1B

3/51

1270	1280	1290	1300	1310	1320
CCGCTGGTGG	CGGCCGACTC	GCTCCTGGAG	CATGTGCGGG	AGGACTTCTC	CGGCCTCCTC
1330	1340	1350	1360	1370	1380
CCTGAGGAGT	TCATCAGCCT	TTCCCCACCC	CACGAGGCC	TCGACTACCA	CTTCGGCCTC
1390	1400	1410	1420	1430	1440
GAGGAGGGCG	AGGGCATCAG	AGACCTCTTC	GACTGTGACT	TTGGGGACCT	CACCCCCCTG
1450	1460	1470	1480	1490	1500
GATTTCTGAC	AGGGCTTGGA	GGGACCAGGG	TTTCCAGAGT	AGCTCACCTT	GTCTCTGCAG
1510	1520	1530	1540	1550	1560
CCCTGGAGCC	CCCTGTCCCT	GGCCGTCTC	CCAGCCTGTT	TGGAAACATT	TAATTTATAC
1570	1580	1590	1600	1610	1620
CCCTCTCTC	TGTCTCCAGA	AGCTTCTAGC	TCTGGGGTCT	GGCTACCGCT	AGGAGGCTGA
1630	1640	1650	1660	1670	1680
GCAAGCCAGG	AAGGGAAGGA	GTCTGTGTGG	TGTGTATGTG	CATGCAGCCT	ACACCCACAC
1690	1700	1710	1720	1730	1740
GTGTGTACCG	GGGGTGAATG	TGTGTGAGCA	TGTGTGTGTG	CATGTACCGG	GGAATGAAGG
1750	1760	1770	1780	1790	1800
TGAACATACA	CCTCTGTGTG	TGCACTGCAG	ACACGCCCCA	GTGTGTCCAC	ATGTGTGTGC
1810	1820	1830	1840	1850	1860
ATGAGTCCAT	CTCTGCGCGT	GGGGGGGCTC	TAAGTGCCT	TTGCGCCCTT	TTGCTCGTGG
1870	1880	1890	1900	1910	1920
GGTCCCACAA	GGCCCAGGGC	AGTGCCTGCT	CCCAGAACT	GGTGCTCTGA	CCAGGCCAGG
1930	1940	1950	1960	1970	1980
TGGGGAGGCT	TTGGCTGGCT	GGGCGTGTAG	GACGGTGAGA	GCACTTCTGT	CTTAAAGGTT
1990	2000	2010	2020	2030	2040
TTTTCTGATT	GAAGCTTTAA	TGGAGCGTTA	TTTATTTATC	GAGGCCTCTT	TGGTGAGCCT
2050	2060	2070	2080	2090	2100
GGGGAATCAG	CAAAAGGGGA	GGAGGGGTGT	GGGGTTGATA	CCCCAACTCC	CTCTACCCTT
2110	2120	2130	2140	2150	2160
GAGCAAGGGC	AGGGGTCCCT	GAGCTGTTCT	TCTGCCCCAT	ACTGAAGGAA	CTGAGGCCTG
2170	2180	2190	2200	2210	2220
GGTGATTTAT	TTATTGGGAA	AGTGAGGGAG	GGAGACAGAC	TGACTGACAG	CCATGGGTGG
2230	2240	2250	2260	2270	2280
TCAGATGGTG	GGGTGGGCCC	TCTCCAGGGG	GCCAGTTCAG	GGCCCAGCTG	CCCCCAGGA
2290	2300	2310	2320	2330	2340
TGGATATGAG	ATGGGAGAGG	TGAGTGGGGG	ACCTTCACTG	ATGTGGGCAG	GAGGGGTGGT
2350	2360	2370	2380	2390	2400
GAAGGCCTCC	CCCAGCCCAG	ACCCTGTGGT	CCCTCCTGCA	GTGTCTGAAG	CGCCTGCCTC
2410	2420	2430	2440	2450	2460
CCCACTGCTC	TGCCCCACCC	TCCAATCTGC	ACTTTGATTT	GCTTCCTAAC	AGCTCTGTTC
2470	2480	2490	2500	2520	2520
CCTCCTGCTT	TGGTTTTAAT	AAATATTTTG	ATGACGTTAA	AAAAAGGAAT	TCGATAT

FIG. 1B
(CONTINUED)

SUBSTITUTE SHEET (RULE 26)

4/51

```

1  ttccggtttt  tctcagggga  cgttgaaatt  atttttgtaa  cgggagtcgg  gagaggacgg
61  ggcgtgcccc  gcgtgcgcgc  gcgtgcgtcc  ccccgccgct  cctccacagc  tcgctggctc
121  ccgccgcgga  aaggcgctcat  gccgcccaaa  acccccgcga  aaacggccgc  caccgccgcc
181  gctgccgcgc  cggaaccccc  ggcaccgcgc  ccgccgcgcc  ctccctgagga  ggaccagag
241  caggacagcg  gcccggagga  cctgcctctc  gtcaggcttg  agtttgaaga  aacagaagaa
301  cctgatttta  ctgcattatg  tcagaaatta  aagataccag  atcatgtcag  agagagagct
361  tgggttaactt  gggagaaagt  ttcattctgt  gatggagtat  tgggaggtta  tattcaaaag
421  aaaaaggaac  tgtgggggaat  ctgtatcttt  attgcagcag  ttgacctaga  tgagatgtcg
481  ttcactttta  ctgagctaca  gaaaaacata  gaaatcagtg  tccataaatt  ctttaactta
541  ctaaaagaaa  ttgataccag  taccaaagtt  gataatgcta  tgtcaagact  gttgaagaag
601  tatgatgtat  tgtttgcact  cttcagcaaa  ttggaaagga  catgtgaact  tatatatttg
661  acacaaccca  gcagttcgat  atctactgaa  ataaattctg  cattgggtgct  aaaagtttct
721  tggatcacat  ttttattagc  taaaggggaa  gtattacaaa  tggaaagtga  tctggtgatt
781  tcatttcagt  taatgctatg  tgtccttgac  tattttatta  aactctcacc  tcccactgtg
841  ctcaaagaac  catataaaac  agctgttata  cccattaatg  gttcacctcg  aacaccagg
901  cgaggtcaga  acaggagtgc  acggatagca  aaacaactag  aaaatgatac  aagaattatt
961  gaagtctctc  gtaaagaaca  tgaatgtaat  atagatgagg  tgaanaatgt  ttatttcaaa
1021  aattttatac  cttttatgaa  ttctcttgga  ctgttaacat  ctaatggact  tccagagggt
1081  gaaaatcttt  ctaaacgata  cgaagaaatt  tatcttaaaa  ataaagatct  agatgcaaga
1141  ttatttttgg  atcatgataa  aactcttcag  actgattcta  tagacagttt  tgaacacag
1201  agaacaccac  gaaaaagtaa  ccttgatgaa  gaggtgaatg  taattcctcc  acacactcca
1261  gttaggactg  ttatgaacac  tatccaacaa  ttaatgatga  ttttaaatc  agcaagtgat
1321  caaccttcag  aaaatctgat  ttcctatatt  aacaactgca  cagtgaatcc  aaaagaaagt
1381  atactgaaaa  gagtgaagga  tataggatac  atctttaaag  agaaatttgc  taaagctgtg
1441  ggacagggtt  gtgtcgaat  tggatcacag  cgatacaaac  ttggagttcg  cttgtattac
1501  cgagtaatgg  aatccatgct  taaatcagaa  gaagaacgat  tatccattca  aaattttagc
1561  aaacttctga  atgacaacat  ttttcatatg  tctttattgg  cgtgcgctct  tgaggttgta
1621  atggccacat  atagcagaag  tacatctcag  aatcttgatt  ctggaacaga  ttgtctttc
1681  ccatggattc  tgaatgtgct  taatttaaaa  gcctttgatt  tttacaaagt  gatcgaaagt
1741  tttatcaaa  cagaaggcaa  cttgacaaga  gaaatgataa  aacatttaga  acgatgtgaa
1801  catcgaatca  tggaaatccct  tgcattggct  tcagattcac  ctttatttga  tcttattaaa
1861  caatcaaagg  accgagaagg  accaactgat  caccttgaat  ctgcttgctc  tcttaatctt
1921  cctctccaga  ataatcacac  tgcagcagat  atgtatcttt  ctctgtaag  atctccaaag
1981  aaaaaagggt  caactacgcg  tgtaaaattc  actgcaaagt  cagagacaca  agcaacctca
2041  gccttccaga  cccagaagcc  attgaaatct  acctctcttt  cactgtttta  taaaaaagtg
2101  tatcggttag  cctatctccg  gctaaataca  ctttgatgaa  gccttctgtc  tgagcaccga
2161  gaattagaac  atatcatctg  gacccttttc  cagcacaccc  tgcagaatga  gtatgaactc
2221  atgagagaca  ggcatttgga  ccaaattatg  atgtgttcca  tgtatggcat  atgcaaagtg
2281  aagaatatag  accttaaat  caaaatcatt  gtaacagcat  acaaggatct  tctcatgct
2341  gttcaggaga  cattcaaacg  tgttttgatc  aaagaagagg  agtatgattc  tattatagta
2401  ttctataact  cggctctcat  gcagagactg  aaaacaaata  ttttgtagta  tgcttccacc
2461  agggccccta  ccttgctcacc  aatacctcac  attcctcgaa  gcccttaca  gtttcttagt
2521  tcacccttac  ggattcctgg  agggaacatc  tatatttcac  ccctgaagag  tccatataaa
2581  atttcagaag  gtctgccaac  accaacaata  atgactccaa  gatcaagaat  cttagtatca
2641  attggtgaat  cattcgggac  ttctgagaag  ttccagaaaa  taaatcagat  ggtatgtaac
2701  agcgaccgtg  tgctcaaaaag  aagtgtgtaa  ggaagcaacc  ctctaaacc  actgaaaaaa
2761  ctacgctttg  atattgaagg  atcagatgaa  gcagatggaa  gtaaacatct  cccaggagag
2821  tccaaatttc  agcagaaact  ggcagaaatg  acttctactc  gaacacgaat  gcaaaagcag
2881  aaaatgaatg  atagcatgga  tacctcaaac  aaggaagaga  aatgaggatc  tcaggacctt
2941  ggtggacact  gtgtacacct  ctggattcat  tgtctctcac  agatgtgact  gtat

```

FIG. 2A

5/51

"MPPKTPRKTAATAAAAAEPPAPPPPPPEEDPEQDSGPEDLPL
VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
IFIAAVDLDEMSFTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKKYDVLFA
LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLAR
LFLDHDKTLQTDSDSFETQRTPRKSNLDEEVNVI PHTPVRTVMNTIQQLMILNSA
SDQPSENLI SYFNNCTVNPKE SILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLG
RLYYRVMESMLKSEERLSIQNF SKLLNDNIFHMSLLACALEVVMATYSRSTSONLDS
GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNLTLCERLLSEHPELEHIWT
LFQHTLQNEYELMRDRHLDQIMCMSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
RVLIKEEEYDSII VFYNSVFMORLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILV SIGESFGTSEKFQKINQMVCNSD
RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQKLAEMTSTRTRMQKQ
KMND SMDTSNKEEK"

FIG. 2B

6/51

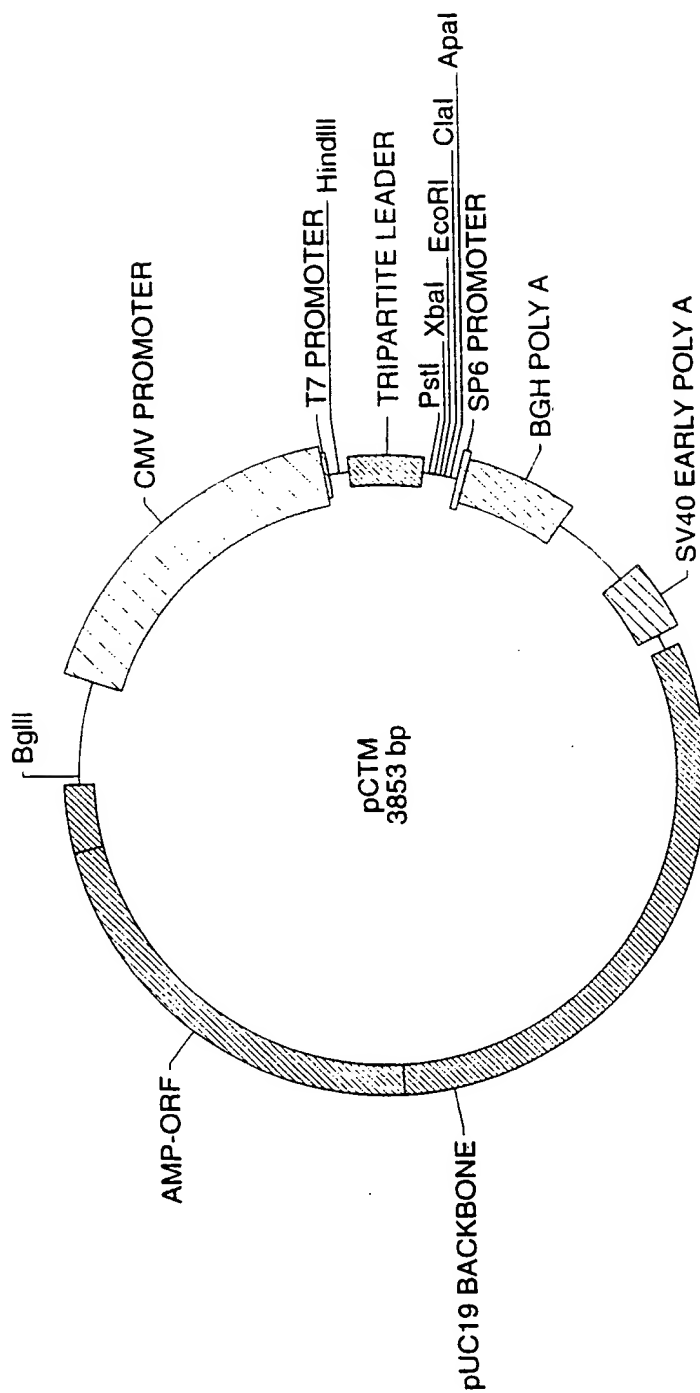


FIG. 3

7/51

```

                                >HincII
                                |
                                >AccI
                                ||
                                >Sali
                                |||
          >BglII
          |
10  |      20      30      40      50      60
*  *  *  *  *  *  *  *  *  *  *  *  *  *
GACGGATCGG GAGATCTCCC GATCCCCTAT GGTGACTCT CAGTACAATC TGCTCTGATG

                                >AlwNI
                                |
70  |      80      90      100     110     120
*  *  *  *  *  *  *  *  *  *  *  *  *
CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG

          >ApoI
          |
130 |      140     150     160     170     180
*  *  *  *  *  *  *  *  *  *  *  *  *
CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC

                                >HincII
                                |
                                >AflIII
                                |
                                >MluI
                                |
          >NruI
          |
190 |      200     210     220     230
*  *  *  *  *  *  *  *  *  *  *  *  *
TTAGGGTTAG GCGTTTTGCG CTGCTTCG CGA TGT ACG GGC CAG ATA TAC GCG TTG
          Arg Cys Thr Gly Gln Ile Tyr Ala Leu>
          ___d___d___CMV PROMOTER___d___d___>

          >SpeI
          |
240 |      250     260     270     280
*  *  *  *  *  *  *  *  *  *  *  *  *
ACA TTG ATT ATT GAC TAG TTA TTA ATA GTA ATC AAT TAC GGG GTC ATT
Thr Leu Ile Ile Asp *** Leu Leu Ile Val Ile Asn Tyr Gly Val Ile>
___d___d___d___d___d___d___CMV PROMOTER___d___d___d___d___d___d___>

290 |      300     310     320     330
*  *  *  *  *  *  *  *  *  *  *  *  *
AGT TCA TAG CCC ATA TAT GGA GTT CCG CGT TAC ATA ACT TAC GGT AAA
Ser Ser *** Pro Ile Tyr Gly Val Pro Arg Tyr Ile Thr Tyr Gly Lys>
___d___d___d___d___d___d___CMV PROMOTER___d___d___d___d___d___d___>

          >BglI
          |
340 |      350     360     370
*  *  *  *  *  *  *  *  *  *  *  *  *
TGG CCC GCC TGG CTG ACC GCC CAA CGA CCC CCG CCC ATT GAC GTC AAT
Trp Pro Ala Trp Leu Thr Ala Gln Arg Pro Pro Pro Ile Asp Val Asn>
___d___d___d___d___d___d___CMV PROMOTER___d___d___d___d___d___d___>

380 |      390     400     410     420
*  *  *  *  *  *  *  *  *  *  *  *  *
AAT GAC GTA TGT TCC CAT AGT AAC GCC AAT AGG GAC TTT CCA TTG ACG
Asn Asp Val Cys Ser His Ser Asn Ala Asn Arg Asp Phe Pro Leu Thr>
___d___d___d___d___d___d___CMV PROMOTER___d___d___d___d___d___d___>

```

FIG. 4

```

>AatII                                     >BglI
430          440          450          460          470
*          *          *          *          *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
_d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_d_d>

>NdeI                                     >AatII
480          490          500          510          520
*          *          *          *          *
AGT GTA TCA TAT GCC AAG TAC GCC CCC TAT TGA CGT CAA TGA CGG TAA
Ser Val Ser Tyr Ala Lys Tyr Ala Pro Tyr *** Arg Gln *** Arg ***>
_d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_d_d>

>BglI
530          540          550          560          570
*          *          *          *          *
ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATG GGA CTT TCC
Met Ala Arg Leu Ala Leu Cys Pro Val His Asp Leu Met Gly Leu Ser>
_d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_d_d>

>BsaAI                                     >NcoI
>SnaBI                                     >StyI   >MslI
580          590          600          610          620
*          *          *          *          *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
_d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_d_d>

620          630          640          650          660
*          *          *          *          *
GCG GTT TTG GCA GTA CAT CAA TGG GCG TGG ATA GCG GTT TGA CTC ACG
Ala Val Leu Ala Val His Gln Trp Ala Trp Ile Ala Val *** Leu Thr>
_d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_d_d>

>AatII                                     >BamI
670          680          690          700          710
*          *          *          *          *
GGG ATT TCC AAG TCT CCA CCC CAT TGA CGT CAA TGG GAG TTT GTT TTG
Gly Ile Ser Lys Ser Pro Pro His *** Arg Gln Trp Glu Phe Val Leu>
_d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_d_d>

720          730          740          750          760
*          *          *          *          *
GCA CCA AAA TCA ACG GGA CTT TCC AAA ATG TCG TAA CAA CTC CGC CCC
Ala Pro Lys Ser Thr Gly Leu Ser Lys Met Ser *** Gln Leu Arg Pro>
_d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_d_d>

770          780          790          800          810
*          *          *          *          *
ATT GAC GCA AAT GGG CGG TAG GCG TGT ACG GTG GGA GGT CTA TAT AAG
Ile Asp Ala Asn Gly Arg *** Ala Cys Thr Val Gly Gly Leu Tyr Lys>
_d_d_d_d_d_d_CMV PROMOTER_d_d_d_d_d_d_d_d>

```

SUBSTITUTE SHEET (RULE 26)

```

>BanII
|
>SacI
|
>BsiHKA I
|
>Ecl136II
|      |      |      |      |      |      |      |
820    830    840    850
*      *      *      *      *      *      *      *
CAG AGC TCT CTG GCT AAC TAG AGA ACC CAC TGC TTA CTG GCT TAT CGA
Gln Ser Ser Leu Ala Asn *** Arg Thr His Cys Leu Leu Ala Tyr Arg>
_d _d _d _d _d _d _d _d CMV PROMOTER _d _d _d _d _d _d _d >

>KpnI
|
>BsaI
|
>Acc65I
|
>AseI
|
>T7_PROMOTER
|
>SfcI
|
>HindIII
|
>BanI
|
860    870    880    890    900    910
*      *      *      *      *      *
AAT T AATACGA CTCACTATAG GGAGACCCAA GCTTCGCGCG GTTACCCTC
Asn Xxx>
_d _>

>PflMI
|
>PvuII
|
>EarI
|
>MspAlI
|
>BanII
|
920    930    940    950    960    970
*      *      *      *      *      *
TCTTCCGCAT CGCTGTCTGC GAGGGCCAGC TGTTGGGCTC GCGGTTGAGG ACAAACTCTT
e _____ TRIPARTITE LEADER SEQUENCE e _____>

>EarI
|
>ScaI
|
980    990    1000    1010    1020    1030
*      *      *      *      *      *
CGCGGTCTTT CCAGTACTCT TGGATCGGAA ACCCGTCGGC CTCCGAACGG TACTCCGCCA
e _____ TRIPARTITE LEADER SEQUENCE e _____>

>SfcI
|
>MspAlI
|
>XhoI
|
>BsiEI
|
>PaeR7I
|
>EaeI
|
>BsoBI
|
>NotI
|
>AvaI
|
>EagI
|
>PpuMI
|
>Eco0109I
|
1040    1050    1060    1070    1080    1090
*      *      *      *      *      *
CCGAGGGACC TGAGCGAGTC CGCATCGACC GGATCGGAAA ACCTCTCGAG GCGGCCGCTG
TRIPARTITE LEADER SEQUENCE e _____>

```

SUBSTITUTE SHEET (RULE 26)

```

>XbaI >ApoI >EcoRV >BspDI >EcoO109I >SfcI >MslI
| | | | | | |
>PstI >EcoRI >BsiWI >BspDI >BanII >MslI
| | | | | | |
| | * 1100 | 1110 | 1120 | 1130 | 1140 |
| | * | * | * | * | * |
CAGTCTAGAC GAATTCGCGT ACGATATCGA TGGGCCCTAT T CTA TAG TGT CAC CTA
Leu *** Cys His Leu
SP6 PROMOTER
>

>BanII
|
>BsiHKA I
|
>SacI
|
>Ecl136II >BclI
| |
>BGH POLY A
| |
1150 | 1160 | 1170 | 1180 | 1190 | 1200
* | * | * | * | * |
AAT G CTAGAGCTCG CTGATCAGCC TCGACTGTGC CTTCTAGTTG CCAGCCATCT
Asn>
____>

>BanI
|
1210 1220 1230 1240 1250 1260
* * * * *
GTTGTTTGCC CCTCCCCGT GCCTTCCTTG ACCCTGGAAG GTGCCACTCC CACTGTCCTT

1270 1280 1290 1300 1310 1320
* * * * *
TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA GGTGTCATTC TATTCTGGGG

>BbsI
|
1330 1340 1350 1360 1370 1380
* * * * *
GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGAAG ACAATAGCCG AAATGACCGA

>BssSI
|
>BspMI
|
1390 1400 1410 1420 1430 1440
* * * * *
CCAAGCGACG CCCAACCTGC CATCACGAGA TTTCGATTCC ACCGCCGCT TCTATGAAAG

>NaeI
|
>BsrFI
|
>BpmI
|
>NgoMI
|
1450 1460 1470 1480 1490 1500
* * * * *
GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG ATCCTCCAGC GCGGGGATCT

```

SUBSTITUTE SHEET (RULE 26)

11/51

```

                                >BpmI
                                |
                                >SV40_early_poly_A
                                |
      1510      1520      1530      1540      1550      1560
      *      *      *      *      *      *
CATGCTGGAG TTCTTCGCCC ACCCCAACCT GTTTATTGCA GCTTATAATG GTTACAAATA

                                >ApoI
                                |
      1570      1580      1590      1600      1610      1620
      *      *      *      *      *      *
AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTTT TCACTGCATT CTAGTTGTGG

                                >BsmI
                                |
                                >HincII
                                |
                                >Bst1107I
                                |
                                >AccI
                                ||
                                >AccI
                                ||
                                >SalI
                                |||
      1630      1640      1650      1660      1670      1680
      *      *      *      *      *      *
TTTGTCCAAA CTCATCAATG TATCTTATCA TGTCTGTATA CCGTCGACCT CTAGCTAGAG
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

                                >BsrBI
                                |
      1690      1700      1710      1720      1730      1740
      *      *      *      *      *      *
CTTGGCGTAA TCATGGTCAT AGCTGTTTCC TGTGTGAAAT TGTTATCCGC TCACAATTCC
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

                                >BamI
                                |
      1750      1760      1770      1780      1790      1800
      *      *      *      *      *      *
ACACAACATA CGAGCCGGAA GCATAAAGTG TAAAGCCTGG GGTGCCTAAT GAGTGAGCTA
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

                                >AseI
                                |
      1810      1820      1830      1840      1850      1860
      *      *      *      *      *      *
ACTCACATTA ATTGCGTTGC GCTCACTGCC CGCTTTCAG TCGGGAAACC TGTCGTGCCA
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

>PvuII
|
>MspAI | >AseI | >EaeI | >HaeII
|      |      |      |
|      *      *      *      *      *      *
|      1870      1880      1890      1900      1910      1920
|      *      *      *      *      *      *
GCTGCATTAA TGAATCGGCC AACGCGCGGG GAGAGGCGGT TTGCGTATTG GGCGCTCTTC
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

>EarI
|
>SapI
|
|      1930      1940      1950      1960      1970      1980
|      *      *      *      *      *      *
CGCTTCCTCG CTCAGTACT CGCTGCGCTC GGTGTTTCGG CTGCGGCGAG CGGTATCAGC
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

```

FIG. 4
(CONTINUED)

12/51

```

                                >AflIII
                                |
      1990      2000      2010      2020      2030      2040
      *      *      *      *      *      *
TCACTCAAAG GCGGTAATAC GGTATCCAC AGAATCAGGG GATAACGCAG GAAAGAACAT
      c      PUC19 BACKBONE H3 TO AATII c      >

      2050      2060      2070      2080      2090      2100
      *      *      *      *      *      *
GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG GCCGCGTTGC TGGCGTTTTT
      c      PUC19 BACKBONE H3 TO AATII c      >

                                >DrdI
                                |
      2110      2120      2130      2140      2150      2160
      *      *      *      *      *      *
CCATAGGCTC CGCCCCCTG ACGAGCATCA CAAAATCGA CGCTCAAGTC AGAGGTGGCG
      c      PUC19 BACKBONE H3 TO AATII c      >

                                >BssSI
                                |
      2170      2180      2190      2200      2210      2220
      *      *      *      *      *      *
AAACCCGACA GGAATAAAA GATACCAGGC GTTCCCCCT GGAAGCTCCC TCGTGCCTC
      c      PUC19 BACKBONE H3 TO AATII c      >

                                >BsaWl
                                |
      2230      2240      2250      2260      2270      2280
      *      *      *      *      *      *
TCCTGTTCCG ACCCTGCCG TTACCGGATA CCGTCCGCC TTTCTCCCTT CGGGAAGCGT
      c      PUC19 BACKBONE H3 TO AATII c      >

      >HaeII      >SfcI
      |      |
      2290      2300      2310      2320      2330      2340
      *      *      *      *      *      *
GGCGCTTTCT CAATGCTCAC GCTGTAGGTA TCTCAGTTCG GTGTAGGTCG TTCGCTCCAA
      c      PUC19 BACKBONE H3 TO AATII c      >

      >BsiHKAI      >MspAlI
      |      |
      >ApaLI      >BsiEI      >BsaWI
      |      |      |
      2350      2360      2370      2380      2390      2400
      *      *      *      *      *      *
GCTGGGCTGT GTGCACGAAC CCCCCGTTCA GCCCGACCGC TGCGCCTTAT CCGGTAACCTA
      c      PUC19 BACKBONE H3 TO AATII c      >

                                >AlwNI
                                |
      2410      2420      2430      2440      2450      2460
      *      *      *      *      *      *
TCGTCTTGAG TCCAACCCGG TAAGACACGA CTTATCGCCA CTGGCAGCAG CCACTGGTAA
      c      PUC19 BACKBONE H3 TO AATII c      >

                                >SfcI
                                |
      2470      2480      2490      2500      2510      2520
      *      *      *      *      *      *
CAGGATTAGC AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTGAAGT GGTGGCCTAA
      c      PUC19 BACKBONE H3 TO AATII c      >

```

FIG. 4
(CONTINUED)

13/51

```

      2530      2540      2550      2560      2570      2580
      *      *      *      *      *      *
CTACGGCTAC ACTAGAAGGA CAGTATTGG TATCTGCGCT CTGCTGAAGC CAGTTACCTT
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

>Eco57I                                >MspAlI
|                                     |
| 2590      2600      2610      2620      2630      2640
| *      *      *      *      *      *
CGGAAAAAGA GTTGGTAGCT CTTGATCCGG CAAACAAACC ACCGCTGGTA GCGGTGGTTT
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

      2650      2660      2670      2680      2690      2700
      *      *      *      *      *      *
TTTTGTTTGC AAGCAGCAGA TTACGCGCAG AAAAAAGGA TCTCAAGAAG ATCCTTTGAT
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

                                                    >BspHI
                                                    |
      2710      2720      2730      2740      2750      2760
      *      *      *      *      *      *
CTTTTCTACG GGGTCTGACG CTCAGTGGAA CGAAACTCA CGTTAAGGGA TTTTGGTCAT
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

                                >DraI                                >DraI
                                |                                |
      2770      2780      2790      2800      2810      2820
      *      *      *      *      *      *
GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

                                                    >BamI
                                                    |
      2830      2840      2850      2860      2870      2880
      *      *      *      *      *      *
AATCTAAAGT ATATATGAGT AACTTGGTC TGACAGTTAC CAATGCTTAA TCAGTGAGGC
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>
                                     a_____AMP-ORF_____>

                                                    >AhdI
                                                    |
      2890      2900      2910      2920      2930      2940
      *      *      *      *      *      *
ACCTATCTCA GCGATCTGTC TATTTGTTTC ATCCATAGTT GCCTGACTCC CCGTCGTGTA
_____a_____a_____AMP-ORF_____a_____a_____>
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

                                                    >BsaI
                                                    |
                                                    >BsrDI    >BpmI
                                                    |
      2950      2960      2970      2980      2990      3000
      *      *      *      *      *      *
GATAACTACG ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA
_____a_____a_____AMP-ORF_____a_____a_____>
_____c_____PUC19 BACKBONE H3 TO AATII_____c_____>

>BsrFI                                >BglI
|                                     |
| 3010      3020      3030      3040      3050      3060
| *      *      *      *      *      *
CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGA GGGCCGAGCG
_____a_____a_____AMP-ORF_____a_____a_____>
_____c_____PUC19 BACKBONE H3 To AATII_____c_____>

```

FIG. 4
(CONTINUED)

14/51

```

                                >AseI
                                |
      3070      3080      3090      3100      3110      3120
      *      *      *      *      *      *
CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAATTGTT GCCGGAAGC
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

                                >Psp1406I
                                |
                                >FspI      >BsrDI      >SfcI
                                |      |      |
      3130      3140      3150      3160      3170      3180
      *      *      *      *      *      *
TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG CTACAGGCAT
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

>MslI                                >BsaWI
|      |      |      |      |      |
      3190      3200      3210      3220      3230      3240
      *      *      *      *      *      *
CGTGGTGTCA CGTCGTCGT TTGGTATGGC TTCATTCAGC TCCGGTCCC AACGATCAAG
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

                                >PvuI
                                |
                                >BsiEI
                                |
      3250      3260      3270      3280      3290      3300
      *      *      *      *      *      *
GCGAGTTACA TGATCCCCCA TGTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

                                >EaeI      >MslI
                                |      |
      3310      3320      3330      3340      3350      3360
      *      *      *      *      *      *
CGTTGTCAGA AGTAAGTTGG CCGCAGTGT ATCACTCATG GTTATGGCAG CACTGCATAA
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

                                >ScaI
                                |
      3370      3380      3390      3400      3410      3420
      *      *      *      *      *      *
TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTCTGTG ACTIGGTGAGT ACTCAACCAA
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

                                >BsiEI
                                |
      3430      3440      3450      3460      3470      3480
      *      *      *      *      *      *
GTCATTCTGA GAATAGTGTA TCGGCGGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

```

FIG. 4
(CONTINUED)

15/51

```

                                >XmnI
                                |
                                >Psp1406I
                                |
                                >DraI  >BsiHKAI
                                |      |
                                3490  3500  3510  3520  3530  3540
                                *      *      *      *      *      *
TAATACCGCG CCACATAGCA GAACCTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

                                >Eco571
                                |
                                >ApaLI
                                |
                                >BssSI
                                |
                                >MspAII
                                |
                                3550  3560  3570  3580  3590  3600
                                *      *      *      *      *      *
GCGAAACTC TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

>BsiHKAI
|
| 3610  3620  3630  3640  3650  3660
| *      *      *      *      *      *
| ACCCAACTGA TCTTCAGCAT CTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAAACAGG
|      a      a      AMP-ORF      a      a      >
|      c      PUC19 BACKBONE H3 TO AATII      c      >

                                >MslI
                                |
                                3670  3680  3690  3700  3710  3720
                                *      *      *      *      *      *
AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG AAATGTTGAA TACTCATACT
      a      a      AMP-ORF      a      a      >
      c      PUC19 BACKBONE H3 TO AATII      c      >

                                >EarI  >SspI
                                |      |
                                3730  3740  3750  3760  3770  3780
                                *      *      *      *      *      *
CTTCCTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA GCGGATACAT
      c      PUC19 BACKBONE H3 TO AATII      c      >

                                >BspHI  >BsrBI
                                |      |
                                3790  3800  3810  3820  3830  3840
                                *      *      *      *      *      *
ATTTGAATGT ATTTAGAAAA ATAAACAAAT AGGGGTTCCG CGCACATTTT CCCGAAAAGT
      c      PUC19 BACKBONE H3 TO AATII      c      >

>HincII
|
>AccI
||
>AatII
||
>SalI
|||
3850 |||
*      *      |||
GCCACCTGAC GTC
      c      >

```

FIG. 4
(CONTINUED)

16/51

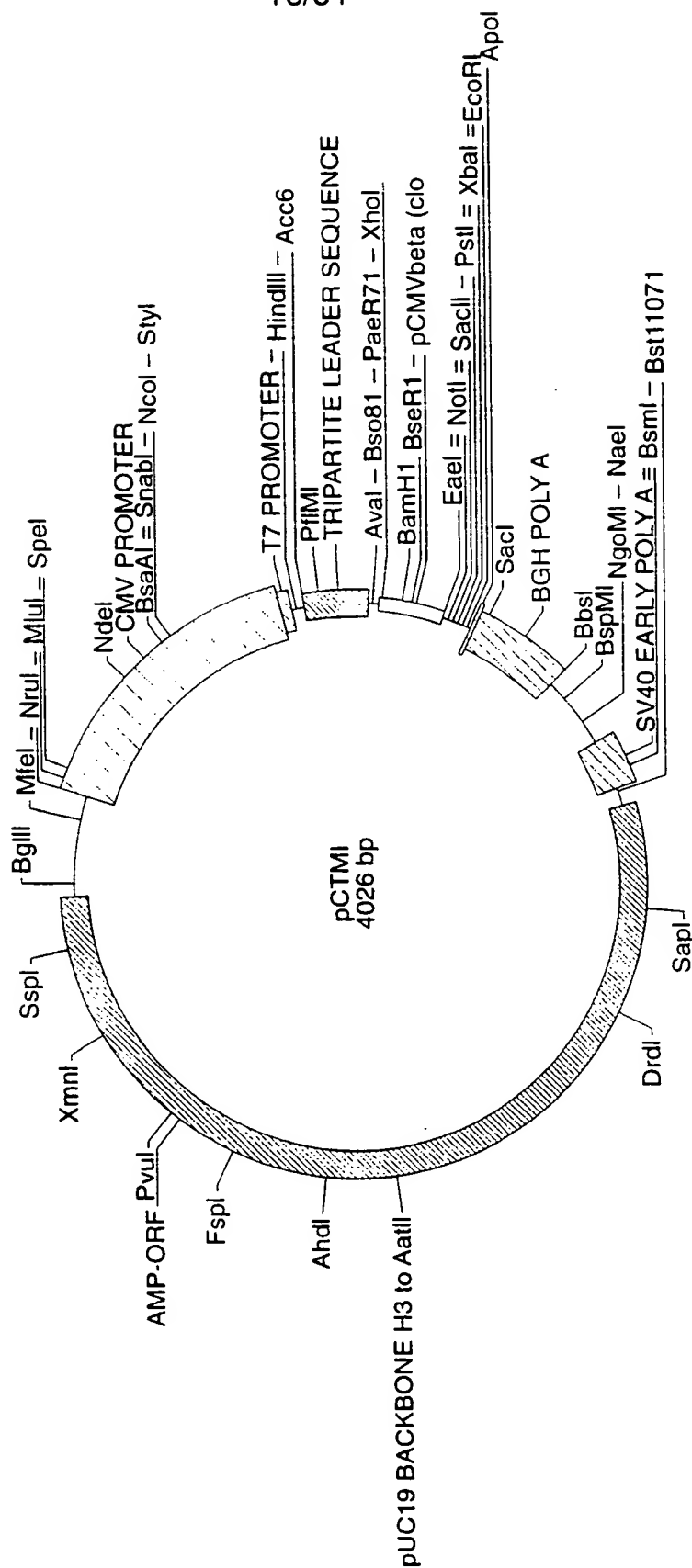


FIG. 5

17/51

```

                                >HincII
                                |
                                >AccI
                                ||
                                >Sall
                                |||
      >BglIII
      |
10  *  |  20  *  30  |  40  *  50  *  60  *
GACGGATCGG GAGATCTCCC GATCCCCTAT GGTCGACTCT CAGTACAATC TGCTCTGATG

                                >AlwNI
                                |
70  *  80  *  90  *  100  *  110  *  120  *
CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG

      >ApoI
      |
130 *  140 *  150 *  160 *  170 *  180 *
CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC

                                                                >HincII
                                                                |
                                                                >AflIII
                                                                |
                                                                >MluI
                                                                |
190 *  200 *  210 *  220 *  230 *
TTAGGGTTAG GCGTTTTGCG CTGCTTCG CGA TGT ACG GGC CAG ATA TAC GCG TTG
      Arg Cys Thr Gly Gln Ile Tyr Ala Leu>
      _e_e_CMV PROMOTER_e_e_e_>

      >SpeI
      |
240 *  250 *  260 *  270 *  280 *
ACA TTG ATT ATT GAC TAG TTA TTA ATA GTA ATC AAT TAC GGG GTC ATT
Thr Leu Ile Ile Asp *** Leu Leu Ile Val Ile Asn Tyr Gly Val Ile>
_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_>

290 *  300 *  310 *  320 *  330 *
AGT TCA TAG CCC ATA TAT GGA GTT CCG CGT TAC ATA ACT TAC GGT AAA
Ser Ser *** Pro Ile Tyr Gly Val Pro Arg Tyr Ile Thr Tyr Gly Lys>
_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_>

      >BglI
      |
340 *  350 *  360 *  370 *
TGG CCC GCC TGG CTG ACC GCC CAA CGA CCC CCG CCC ATT GAC GTC AAT
Trp Pro Ala Trp Leu Thr Ala Gln Arg Pro Pro Pro Ile Asp Val Asn>
_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_>

380 *  390 *  400 *  410 *  420 *
AAT GAC GTA TGT TCC CAT AGT AAC GCC AAT AGG GAC TTT CCA TTG ACG
Asn Asp Val Cys Ser His Ser Asn Ala Asn Arg Asp Phe Pro Leu Thr>
_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_>

```

FIG. 6

```
>AatII                                     >BglI
|                                           |
430           440           450           460           470
*             *             *             *             *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
_e_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_e_e_e_e_>

>NdeI                                     >AatII
|                                           |
480           490           500           510           520
*             *             *             *             *
AGT GTA TCA TAT GCC AAG TAC GCC CCC TAT TGA CGT CAA TGA CGG TAA
Ser Val Ser Tyr Ala Lys Tyr Ala Pro Tyr *** Arg Gln *** Arg ***>
_e_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_e_e_e_e_>

>BglI
|
530           540           550           560           570
*             *             *             *             *
ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATG GGA CTT TCC
Met Ala Arg Leu Ala Leu Cys Pro Val His Asp Leu Met Gly Leu Ser>
_e_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_e_e_e_e_>

>BsaAI                                     >NcoI
|                                           |
>SnaBI                                     >StyI >MslI
|                                           |
580           590           600           610           620
*             *             *             *             *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
_e_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_e_e_e_e_>

620           630           640           650           660
*             *             *             *             *
GCG GTT TTG GCA GTA CAT CAA TGG GCG TGG ATA GCG GTT TGA CTC ACG
Ala Val Leu Ala Val His Gln Trp Ala Trp Ile Ala Val *** Leu Thr>
_e_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_e_e_e_e_>

>AatII                                     >BamHI
|                                           |
670           680           690           700           710
*             *             *             *             *
GGG ATT TCC AAG TCT CCA CCC CAT TGA CGT CAA TGG GAG TTT GTT TTG
Gly Ile Ser Lys Ser Pro Pro His *** Arg Gln Trp Glu Phe Val Leu>
_e_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_e_e_e_e_>

720           730           740           750           760
*             *             *             *             *
GCA CCA AAA TCA ACG GGA CTT TCC AAA ATG TCG TAA CAA CTC CGC CCC
Ala Pro Lys Ser Thr Gly Leu Ser Lys Met Ser *** Gln Leu Arg Pro>
_e_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_e_e_e_e_>

770           780           790           800           810
*             *             *             *             *
ATT GAC GCA AAT GGG CGG TAG GCG TGT ACG GTG GGA GGT CTA TAT AAG
Ile Asp Ala Asn Gly Arg *** Ala Cys Thr Val Gly Gly Leu Tyr Lys>
_e_e_e_e_e_e_e_CMV PROMOTER_e_e_e_e_e_e_e_e_e_e_>
```

SUBSTITUTE SHEET (RULE 26)

19/51

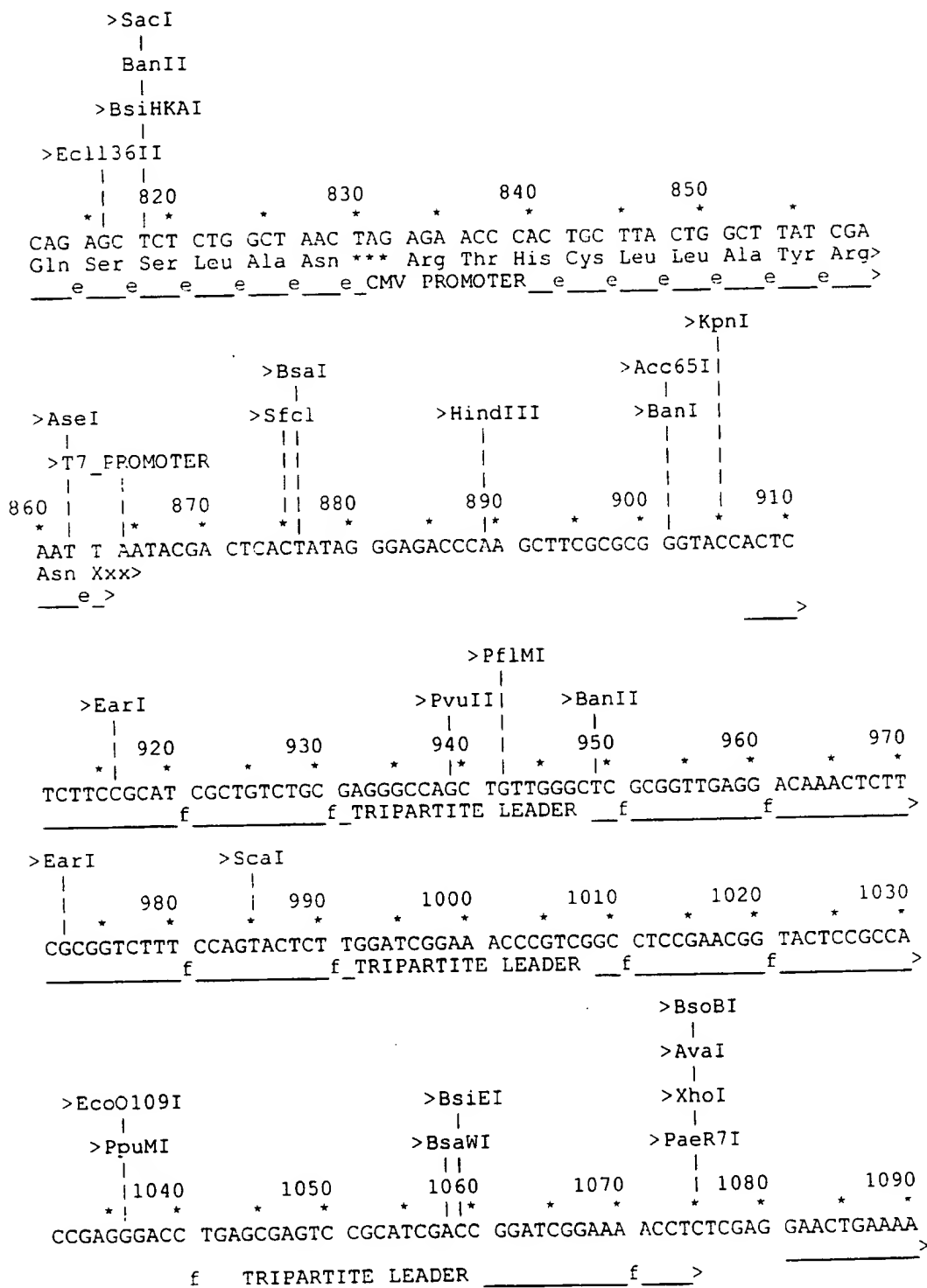


FIG. 6
(CONTINUED)

20/51

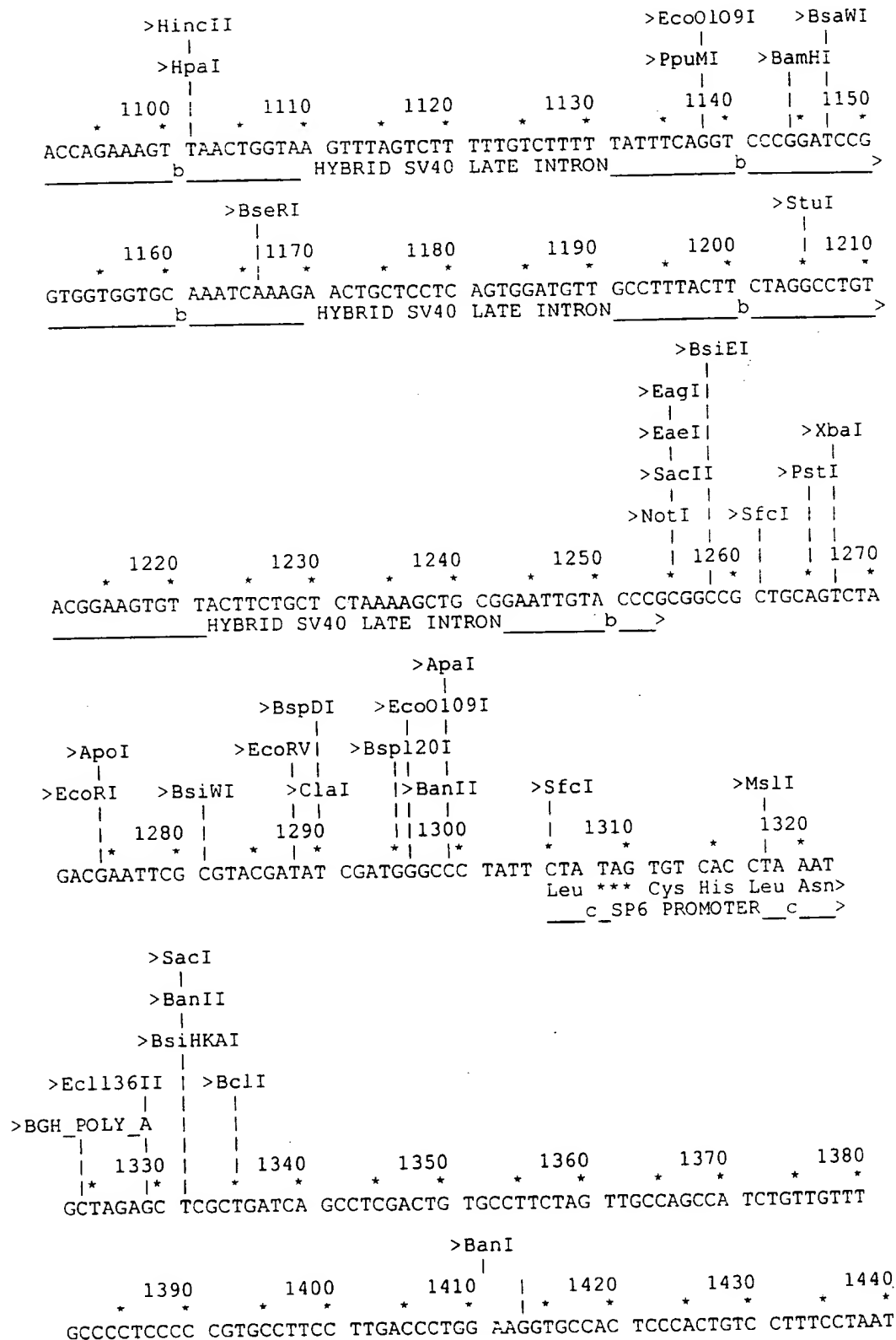


FIG. 6
(CONTINUED)

21/51

```

      1450      1460      1470      1480      1490      1500
      *        *        *        *        *        *
AAAATGAGGA AATTGCATCG CATTGTCTGA GTAGGTGTCA TTCTATTCTG GGGGGTGGGG

                                >BbsI
                                |
      1510      1520      1530      1540      1550      1560
      *        *        *        *        *        *
TGGGGCAGGA CAGCAAGGGG GAGGATTGGG AAGACAATAG CCGAAATGAC CGACCAAGCG

      >BspMI
      |
      >BssSI
      |
      1570      1580      1590      1600      1610      1620
      *        *        *        *        *        *
ACGCCCCAACC TGCCATCAGG AGATTTCGAT TCCACCGCCG CCTTCTATGA AAGGTTGGGC

                                >NaeI
                                |
                                >NgoMI
                                |
                                >BpmI
                                |
                                >BsrFI
                                |
      1630      1640      1650      1660      1670      1680
      *        *        *        *        *        *
TTCGGAATCG TTTCCGGGA CGCCGGCTGG ATGATCCTCC AGCGCCGGGA TCTCATGCTG

                                >BpmI
                                |
                                >SV40_early_poly_A
                                |
      1690      1700      1710      1720      1730      1740
      *        *        *        *        *        *
GAGTTCTTCG CCCACCCCAA CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT

      >ApoI                                >BsmI
      |                                |
      1750      1760      1770      1780      1790      1800
      *        *        *        *        *        *
AGCATCACAA ATTCACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTGTGCC

                                >HincII
                                |
                                >Bst1107I  >AccI
                                |          |
                                >AccI    >SalI
                                |          |
      1810      1820      1830      1840      1850      1860
      *        *        *        *        *        *
AAACTCATCA ATGTATCTTA TCATGTCTGT ATACCGTCGA CCTCTAGCTA GAGCTTGGCG
                                >
                                >BsrBI
                                |
      1870      1880      1890      1900      1910      1920
      *        *        *        *        *        *
TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC CGCTCACAAT TCCACACAAC
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

```

FIG. 6
(CONTINUED)

22/51

```

                                >BamI
                                |
      1930      1940      1950      1960      1970      1980
      *      *      *      *      *      *
ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG CTAAC TCACA
      d      d      PUC19 BACKBONE      d      d      >
                                >AseI
                                |
>AseI                                >PvuII
|                                |
      1990      2000      2010      2020      2030      2040
      *      *      *      *      *      *
TTAATTGCGT TGCGCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT
      d      d      PUC19 BACKBONE      d      d      >
                                >EaeI
                                |
                                >HaeII
                                |
                                >SapI
                                |
      2050      2060      2070      2080      2090      2100
      *      *      *      *      *      *
TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTCGCGTA TTGGGCGCTC TTCCGCTTCC
      d      d      PUC19 BACKBONE      d      d      >
                                >BsiEI
                                |
                                >BsrBI
                                |
      2110      2120      2130      2140      2150      2160
      *      *      *      *      *      *
TCGCTCACTG ACTCGCTGCG CTCGGTTCGT CCGCTGCGGC GAGCGGTATC AGCTCACTCA
      d      d      PUC19 BACKBONE      d      d      >
                                >AflIII
                                |
      2170      2180      2190      2200      2210      2220
      *      *      *      *      *      *
AAGGCGGTAA TACGGTTATC CACAGAATCA GGGGATAACG CAGGAAAGAA CATGTGAGCA
      d      d      PUC19 BACKBONE      d      d      >
      2230      2240      2250      2260      2270      2280
      *      *      *      *      *      *
AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT TGCTGGCGTT TTTCCATAGG
      d      d      PUC19 BACKBONE      d      d      >
                                >DrdI
                                |
      2290      2300      2310      2320      2330      2340
      *      *      *      *      *      *
CTCCGCCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA GTCAGAGGTG GCGAAACCCG
      d      d      PUC19 BACKBONE      d      d      >
                                >BssSI
                                |
      2350      2360      2370      2380      2390      2400
      *      *      *      *      *      *
ACAGGACTAT AAAGATACCA GGCGTTTCCC CCTGGAAGCT CCCTCGTGCG CTCTCCTGTT
      d      d      PUC19 BACKBONE      d      d      >

```

FIG. 6
(CONTINUED)

23/51

```

                >BsaWI
                |
      2410      2420      2430      2440      2450      2460
      *      *      *      *      *      *
      CCGACCCTGC CGCTTACCGG ATACCTGTCC GCCTTCTCC CTTCCGGAAG CGTGGCGCTT
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

                >SfcI
                |
      2470      2480      2490      2500      2510      2520
      *      *      *      *      *      *
      TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

      >BsiHKAI
      |
    >ApaLI|
      |      |
      2530      2540      2550      2560      2570      2580
      *      *      *      *      *      *
      TGTGTGCACG AACCCCCCGT TCAGCCCGAC CGCTGCGCCT TATCCGGTAA CTATCGTCTT
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

                                >BsiEI
                                |
                                >BsaWI
                                |
      2590      2600      2610      2620      2630      2640
      *      *      *      *      *      *
      GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG TAACAGGATT
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

                                >AlwNI
                                |
      2590      2600      2610      2620      2630      2640
      *      *      *      *      *      *
      GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG TAACAGGATT
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

                >SfcI
                |
      2650      2660      2670      2680      2690      2700
      *      *      *      *      *      *
      AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA AGTGGTGGCC TAACTACGGC
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

                                >Eco57I
                                |
      2710      2720      2730      2740      2750      2760
      *      *      *      *      *      *
      TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC CTTCCGAAAA
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

      2770      2780      2790      2800      2810      2820
      *      *      *      *      *      *
      AGAGTTGGTA GCTCTTGATC CGGCAAACAA ACCACCGCTG GTAGCGGTGG TTTTTTGT
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

      2830      2840      2850      2860      2870      2880
      *      *      *      *      *      *
      TGCAAGCAGC AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

                                >BspHI
                                |
      2890      2900      2910      2920      2930      2940
      *      *      *      *      *      *
      ACGGGGTCTG ACGCTCAGTG GAACGAAAC TCACGTTAAG GGATTTTGGT CATGAGATTA
      _____d_____d_____PUC19 BACKBONE_____d_____d_____>

```

FIG. 6
(CONTINUED)

24/51

```

                >DraI                >DraI
                |                |
      2950      2960      2970      2980      2990      3000
      *          *          *          *          *          *
TCAAAAAGGA TCTTCACCTA GATCCTTTTA AATTAAAAAT GAAGTTTAA ATCAATCTAA
      d      d      PUC19 BACKBONE      d      d      >

                                >BamI
                                |
      3010      3020      3030      3040      3050      3060
      *          *          *          *          *          *
AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT TAATCAGTGA GGCACCTATC
      d      d      PUC19 BACKBONE      d      d      >
                                a      AMP-ORF      a      >

                                >AhdI
                                |
      3070      3080      3090      3100      3110      3120
      *          *          *          *          *          *
TCAGCGATCT GTCTATTTTCG TTCATCCATA GTTGCTGAC TCCCGTCGT GTAGATAACT
      a      a      AMP-ORF      a      a      >
      d      d      PUC19 BACKBONE      d      d      >

                                >BsaI
                                |
                                >BsrDI      >BpmI
                                |      |      |
      3130      3140      3150      3160      3170      3180
      *          *          *          *          *          *
ACGATACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA TGATACCGCG AGACCCACGC
      a      a      AMP-ORF      a      a      >
      d      d      PUC19 BACKBONE      d      d      >

>BsrFI                                >BglI
|                                |
      3190      3200      3210      3220      3230      3240
      *          *          *          *          *          *
TCACCGGCTC CAGATTTATC AGCAATAAAC CAGCCAGCCG GAAGGGCCGA GCGCAGAAGT
      a      a      AMP-ORF      a      a      >
      d      d      PUC19 BACKBONE      d      d      >

                                >AseI
                                |
      3250      3260      3270      3280      3290      3300
      *          *          *          *          *          *
GGTCCTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT GTTGCCGGA AGCTAGAGTA
      a      a      AMP-ORF      a      a      >
      d      d      PUC19 BACKBONE      d      d      >

                                >Psp1406I
                                |
                                >FspI      >BsrDI      >SfcI      >MslI
                                |      |      |      |
      3310      3320      3330      3340      3350      3360
      *          *          *          *          *          *
AGTAGTTCGC CAGTTAATAG TTTGCGCAAC GTTGTGCCA TTGCTACAGG CATCGTGCTG
      a      a      AMP-ORF      a      a      >
      d      d      PUC19 BACKBONE      d      d      >

```

FIG. 6
(CONTINUED)

25/51

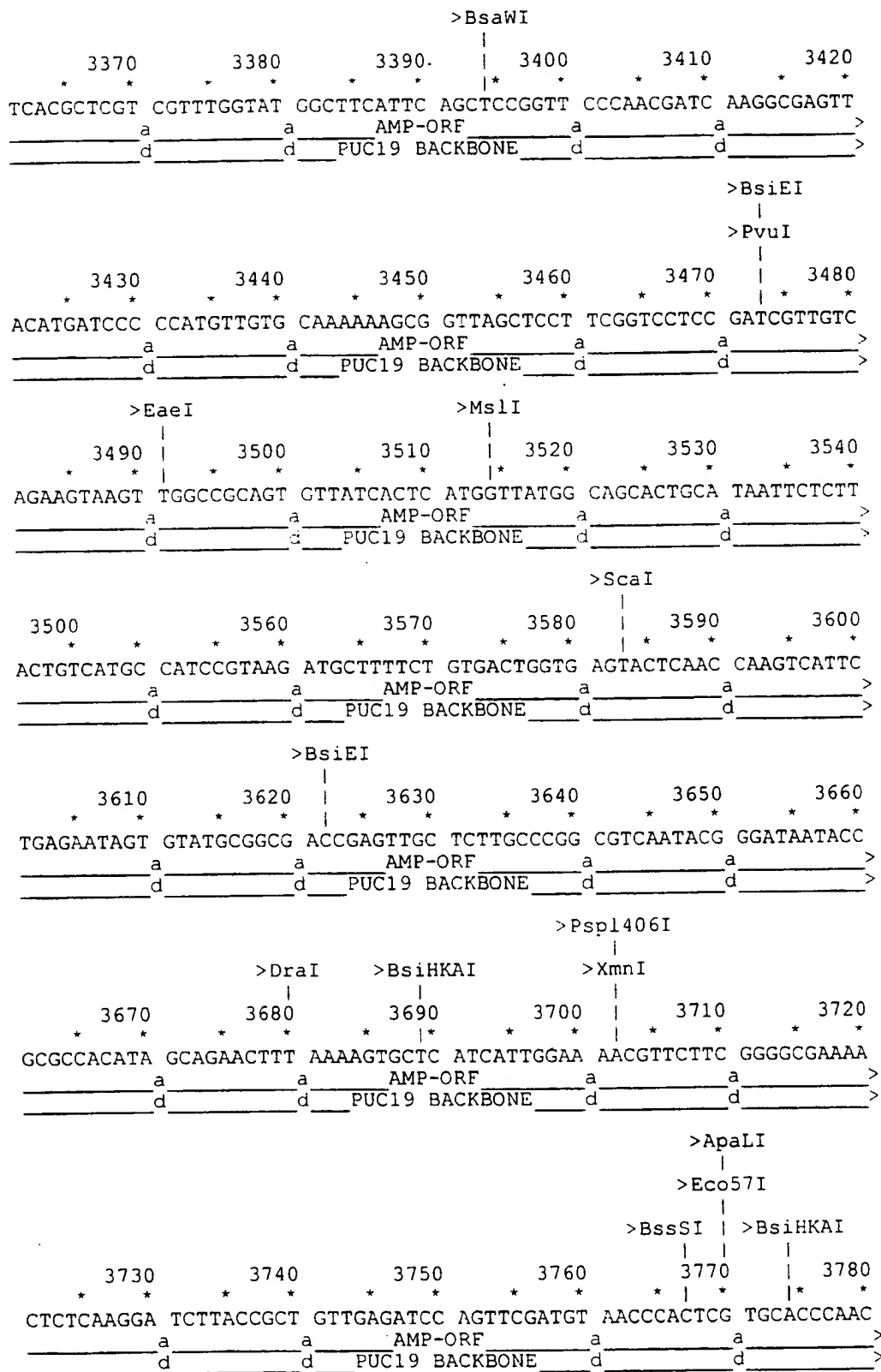


FIG. 6
(CONTINUED)

26/51

```

      3790      3800      3810      3820      3830      3840
      *      *      *      *      *      *
TGATCTTCAG CATCTTTTAC TTTCACCAGC GTTTCTGGGT GAGCAAAAAC AGGAAGGCAA
      a      a      AMP-ORF      a      a      >
      d      d      PUC19 BACKBONE      d      d      >

                                >MslI                                >EarI
                                |                                |
      3850      3860      3870      3880      3890      3900
      *      *      *      *      *      *
AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT GAATACTCAT ACTCTTCCTT
      a      a      AMP-ORF      a      a      >
      d      d      PUC19 BACKBONE      d      d      >

      >SspI                                >BspHI      >BsrBI
      |                                |      |
      3910      3920      3930      3940      3950      3960
      *      *      *      *      *      *
TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA TGAGCGGATA CATATTTGAA
      d      d      PUC19 BACKBONE      d      d      >

      3970      3980      3990      4000      4010      4020
      *      *      *      *      *      *
TGTATTTAGA AAAATAAACA AATAGGGGTT CCGCGCACAT TTCCCCGAAA AGTGCCACCT
      d      d      PUC19 BACKBONE      d      d      >

      >HincII
      |
      >AatII
      ||
      >AccI
      ||
      >SalI
      |||
      |*|
GACGTC
      >

```

FIG. 6
(CONTINUED)

27/51

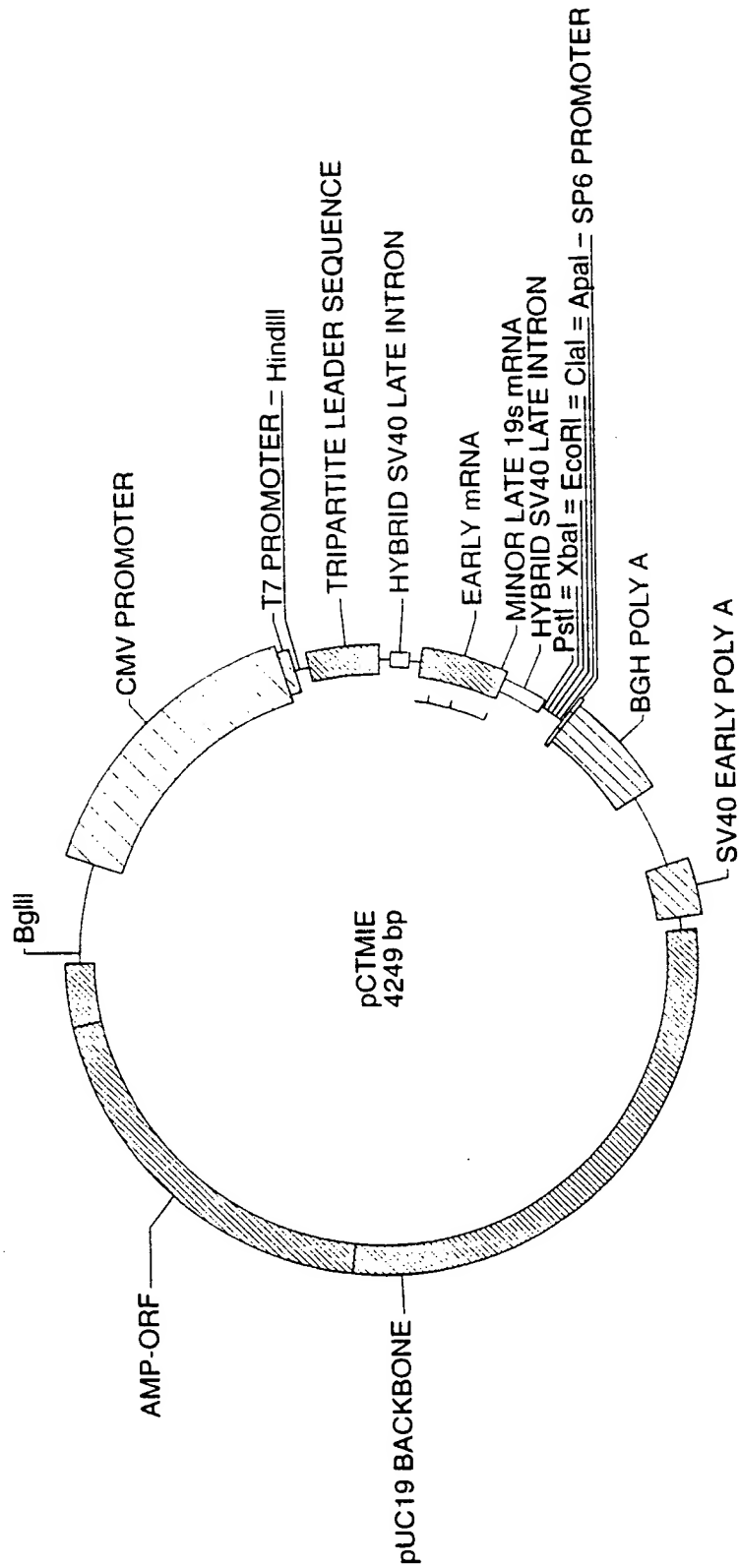


FIG. 7


```

                                >HincII
                                |
                                >AccI
                                ||
                                >SalI
                                |||
>BglII                         ||||
   |                           ||||
10 |                           ||||      40      50      60
* | * * * * * * * * * * * * * * * * * *
GACGGATCGG GAGATCTCCC GATCCCCCTAT GGTCGACTCT CAGTACAATC TGCTCTGATG

                                >AlwNI
                                |
70 *      80 *      90 *     100 *    110 *    120 *
CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG

                                >ApoI
                                |
130 *      140 *     150 *     160 *    170 *    180 *
CGAGCAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC

                                >MfeI
                                |
                                >HincII
                                |
                                >AflIII
                                |
                                >MluI
                                |
                                >NruI
                                |
190 *      200 *     210 *     220 *    230 *    240 *
TTAGGGTTAG GCGTTTTGCG CTGCTTCG CGA TGT ACG GGC CAG ATA TAC GCG TTG
Arg Cys Thr Gly Gln Ile Tyr Ala Leu>
__f__f__CMV PROMOTER__f__f__>

                                >SpeI
                                |
                                >AseI
                                |
240 *      250 *     260 *     270 *    280 *
ACA TTG ATT ATT GAC TAG TTA TTA ATA GTA ATC AAT TAC GGG GTC ATT
Thr Leu Ile Ile Asp *** Leu Leu Ile Val Ile Asn Tyr Gly Val Ile>
__f__f__f__f__f__f__f__CMV PROMOTER__f__f__f__f__f__f__f__>

290 *      300 *     310 *     320 *    330 *
AGT TCA TAG CCC ATA TAT GGA GTT CCG CGT TAC ATA ACT TAC GGT AAA
Ser Ser *** Pro Ile Tyr Gly Val Pro Arg Tyr Ile Thr Tyr Gly Lys>
__f__f__f__f__f__f__f__CMV PROMOTER__f__f__f__f__f__f__f__>

                                >BglI
                                |
                                >AatII
                                |
340 *      350 *     360 *     370 *    380 *
TGG CCC GCC TGG CTG ACC GCC CAA CGA CCC CCG CCC ATT GAC GTC AAT
Trp Pro Ala Trp Leu Thr Ala Gln Arg Pro Pro Pro Ile Asp Val Asn>
__f__f__f__f__f__f__f__CMV PROMOTER__f__f__f__f__f__f__f__>

390 *      400 *     410 *     420 *
AAT GAC GTA TGT TCC CAT AGT AAC GCC AAT AGG GAC TTT CCA TTG ACG
Asn Asp Val Cys Ser His Ser Asn Ala Asn Arg Asp Phe Pro Leu Thr>
f__f__f__f__f__f__f__CMV PROMOTER__f__f__f__f__f__f__f__>

```

FIG. 8

```
>AatII                               >BglI
|                                     |
430             440           450         460       470
*               *              *            *          *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
__f__f__f__f__f__f__f_CMV PROMOTER__f__f__f__f__f__f__f__>

      >NdeI                           >AatII
      |                             |
    480     490        500        510   520
      *       *         *          *      *
AGT GTA TCA TAT GCC AAG TAC GCC CCC TAT TGA CGT CAA TGA CGG TAA
Ser Val Ser Tyr Ala Lys Tyr Ala Pro Tyr *** Arg Gln *** Arg ***>
__f__f__f__f__f__f__f_CMV PROMOTER__f__f__f__f__f__f__f__>

      >BglI
      |
    530     540        550        560       570
      *       *         *          *      *
ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATG GGA CTT TCC
Met Ala Arg Leu Ala Leu Cys Pro Val His Asp Leu Met Gly Leu Ser>
__f__f__f__f__f__f__f_CMV PROMOTER__f__f__f__f__f__f__f__>

                                >BsaAI
                                |
                              >SnaBI
                                |
    580     590        600        610       620
      *       *         *          *      *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
__f__f__f__f__f__f__f_CMV PROMOTER__f__f__f__f__f__f__f__>

                                >StyI
                                |
                              >NcoI   >MslI
                                |       |
    620     630        640        650       660
      *       *         *          *      *
GCG GTT TTG GCA GTA CAT CAA TGG GCG TGG ATA GCG GTT TGA CTC ACG
Ala Val Leu Ala Val His Gln Trp Ala Trp Ile Ala Val *** Leu Thr>
__f__f__f__f__f__f__f_CMV PROMOTER__f__f__f__f__f__f__f__>

                                      >AatII                                  >BanI
                                      |                                           |
    670     680        690        700       710
      *       *         *          *      *
GGG ATT TCC AAG TCT CCA CCC CAT TGA CGT CAA TGG GAG TTT GTT TTG
Gly Ile Ser Lys Ser Pro Pro His *** Arg Gln Trp Glu Phe Val Leu>
__f__f__f__f__f__f__f_CMV PROMOTER__f__f__f__f__f__f__f__>

    720     730        740        750       760
      *       *         *          *      *
GCA CCA AAA TCA ACG GGA CTT TCC AAA ATG TCG TAA CAA CTC CGC CCC
Ala Pro Lys Ser Thr Gly Leu Ser Lys Met Ser *** Gln Leu Arg Pro>
__f__f__f__f__f__f__f_CMV PROMOTER__f__f__f__f__f__f__f__>

    770     780        790        800       810
      *       *         *          *      *
ATT GAC GCA AAT GGG CGG TAG CGG TGT ACG GTG GGA GGT CTA TAT AAG
Ile Asp Ala Asn Gly Arg *** Ala Cys Thr Val Gly Gly Leu Tyr Lys>
__f__f__f__f__f__f__f_CMV PROMOTER__f__f__f__f__f__f__f__>
```

FIG. 8
(CONTINUED)

```
>BsiHKA I
|
SacI
|
BanII
|
>Ecll136 II
|      |      |      |      |
820    830    840    850
* * *   * * *   * * *   * * *
CAG AGC TCT CTG GCT AAC TAG AGA ACC CAC TGC TTA CTG GCT TAT CGA
Gln Ser Ser Leu Ala Asn *** Arg Thr His Cys Leu Leu Ala Tyr Arg>
___f___f___f___f___f___f___f_CMV PROMOTER___f___f___f___f___f___>

                                     >KpnI
                                         |
                                >BsaI          >BanI
                                |              |
                    >SfcI                >Acc65I
                    ||                  ||||
>AseI             >T7_PROMOTER           ||||
|               |                       ||||
>T7_PROMOTER     |                       ||||
|               |                       ||||
860            870            880            890            900            910
* | | | | *         * | | | | *         * | | | | *         * | | | | *
AAT T AATACGA CTC ACT ATAG GGAGACCCAA GCTTCGCGCG GGTACC ACTC
Asn Xxx>
___f_>

                                               >PflMI
                                                    |
                    >EarI                      >PvuII       >BanII
                    |                          |             |
                    * | 920                 * | 940        * | 950
                    * | *                   * | *          * | *
TCTTCCGCAT CGTGTTCTGC GAGGGCCAGC TGTTGGGCTC GCGGTTGAGG ACAACTCTT
_____g____TRIPARTITE LEADER SEQUENCE_____g_____>

>EarI                     >ScaI
|                           |
| 980                     990         1000         1010         1020         1030
| * * * * * * * * * * * * * * * *
CGCGGTCTTT CCAGTACTCT TGGATCGGAA ACCCGTCGGC CTCCGAACGG TACTCCGCCA
_____g____TRIPARTITE LEADER SEQUENCE_____g_____>

                                           >XhoI
                                           |
                                           >AvaI
                                           |
                                   >BsoBI
                                   |
                                   >PaeR7I
                                   |
>EcoO109I                         >BsiEI
|                                 |
>PpuMI                            >BsaWI
|                               ||
| 1040                        1050      1060        1070        1080        1090
* | * * * * * * * * * * * * * * * *
CCGAGGGACC TGAGCGAGTC CGCATCGACC GGATCGGAAA ACCTCTCGAG GAACTGAAAA
```

FIG. 8
(CONTINUED)

31/51

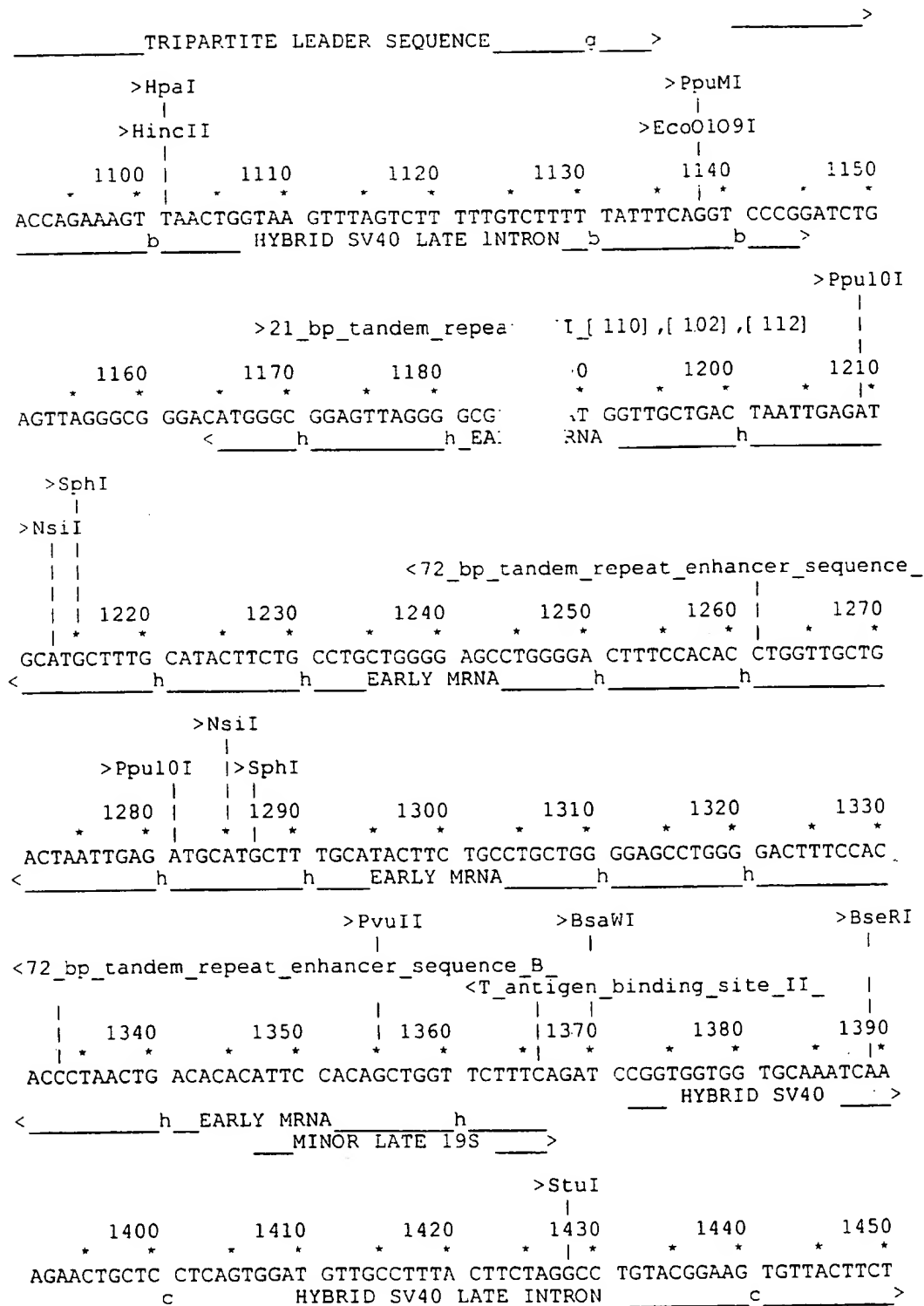


FIG. 8
(CONTINUED)

32/51

```

                                >BsiEI
                                |
                                >NotI
                                |
                                >EaeI
                                |
                                >SacII
                                |
                                >EagI
                                |
                                >SfcI
                                |
                                >XbaI
                                |
                                >PstI
                                |
                                >EcoRI
                                |
                                >ApoI
                                |
                                >BsiWI
                                |
1460      1470      1480      1490      1500      1510
*      *      *      *      *      *
GCTCTAAAAG CTGCGGAATT GTACCCGCGG CCGCTGCAGT CTAGACGAAT TCGCGTACGA
___ HYBRID SV40 LATE INT ___>

                                >ApaI
                                |
                                >BspDI
                                |
                                >ClaI
                                |
                                >EcoRV
                                |
                                >BspI20I
                                |
                                >SfcI
                                |
                                >MslI
                                |
                                >Ecl136II
                                |
                                >BclI
                                |
                                >BspDI
                                |
                                >BanII
                                |
                                >EcoO109I
                                |
                                >BspI20I
                                |
                                >SfcI
                                |
                                >MslI
                                |
                                >Ecl136II
                                |
                                >BclI
                                |
                                >BGH_POLY_A
                                |
                                >BspDI
                                |
                                >BanII
                                |
                                >EcoRV
                                |
                                >BspI20I
                                |
                                >SfcI
                                |
                                >MslI
                                |
                                >Ecl136II
                                |
                                >BclI
                                |
1520      1530      1540      1550      1560
*      *      *      *      *
TATCGATGGG CCCTATT CTA TAG TGT CAC CTA AAT GCTAG AGCTCGCTGA
Leu *** Cys His Leu Asn>
___d_SP6 PROMOTER_d___>

1570      1580      1590      1600      1610      1620
*      *      *      *      *      *
TCAGCCTCGA CTGTGCCTTC TAGTTGCCAG CCACTCTGTTG TTTGCCCTC CCCCCTGCCT

                                >BanI
                                |
1630      1640      1650      1660      1670      1680
*      *      *      *      *      *
TCCTTGACCC TGGAAGGTGC CACTCCCACT GTCCTTTCCT AATAAAATGA GGAAATTGCA

1690      1700      1710      1720      1730      1740
*      *      *      *      *      *
TCGCATTGTC TGAGTAGGTG TCATTCTATT CTGGGGGGTG GGGTGGGGCA GGACAGCAAG

                                >BspMI
                                |
                                >BbsI
                                |
                                >BssSI
                                |
1750      1760      1770      1780      1790      1800
*      *      *      *      *      *
GGGGAGGATT GGGAAGACAA TAGCCGAAAT GACCGACCAA GCGACGCCCA ACCTGCCATC

1810      1820      1830      1840      1850      1860
*      *      *      *      *      *
ACGAGATTTC GATTCCACCG CCGCCTTCTA TGAAAGGTTG GGCTTCGGAA TCGTTTTCCG

```

FIG. 8
(CONTINUED)

33/51

```

>NaeI
|
>BpmI
|
>BsrFI
|
NcoMI
|
1870      1880      1890      1900      1910      1920
* | *      * | *      * | *      * | *      * | *
GGACGCCGGC TGGATGATCC TCCAGCGCGG GGATCTCATG CTGGAGTTCT TCGCCACCCC

>BpmI
|
>SV40_early_poly_A
|
1930      1940      1950      1960      1970      1980
* | *      * | *      * | *      * | *      * | *
CAACTTGTTT ATTGCAGCTT ATAATGGTTA CAAATAAAGC AATAGCATCA CAAATTCAC

>BsmI
|
1990      2000      2010      2020      2030      2040
* | *      * | *      * | *      * | *      * | *
AAATAAAGCA TTTTTCAC TGCATTCTAG TTGTGGTTTG TCCAACTCA TCAATGTATC

>HincII
|
>Bst1107I
|
>AccI
|
>AccI
|
>SalI
|
2050      2060      2070      2080      2090      2100
* | *      * | *      * | *      * | *      * | *
TTATCATGTC TGTATACCGT CGACCTCTAG CTAGAGCTTG GCGTAATCAT GGTCATAGCT
PUC19 BACKBONE >

>BsrBI
|
2110      2120      2130      2140      2150      2160
* | *      * | *      * | *      * | *      * | *
GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG CCGGAAGCAT
PUC19 BACKBONE >

>BamI
|
2170      2180      2190      2200      2210      2220
* | *      * | *      * | *      * | *      * | *
AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG CGTTGCGCTC
PUC19 BACKBONE >

>PvuII
|
>AseI
|
>EaeI
|
2230      2240      2250      2260      2270      2280
* | *      * | *      * | *      * | *      * | *
ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAAATGA TCGGCCAACG
PUC19 BACKBONE >

```

FIG. 8
(CONTINUED)

34/51

```

                                >SapI
                                |
                                >HaeII  >EarI
                                |    |
                2290      2300      2310 | 2320      2330      2340
                *      *      *      | *      *      *
CGCGGGGAGA GGCGGTTTGC GTATTGGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT
                e      e      e PUC19 BACKBONE e      e      e
                                >BsiEI
                                |
                2350      2360      2370 | 2380      2390      2400
                *      *      *      | *      *      *
GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT
                e      e      e PUC19 BACKBONE e      e      e
                                >AflIII
                                |
                2410      2420      2430 | 2440      2450      2460
                *      *      *      | *      *      *
ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGGC
                e      e      e PUC19 BACKBONE e      e      e
                2470      2480      2490 | 2500      2510      2520
                *      *      *      | *      *      *
CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC CCCCTGACGA
                e      e      e PUC19 BACKBONE e      e      e
                                >DrdI
                                |
                2530      2540 | 2550      2560      2570      2580
                *      *      | *      *      *      *
GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA
                e      e      e PUC19 BACKBONE e      e      e
                                >BssSI
                                |
                2590      2600 | 2610      2620      2630      2640
                *      *      | *      *      *      *
CCAGGCGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TGCCGCTTAC
                e      e      e PUC19 BACKBONE e      e      e
                                >HaeII
                                |
                2650      2660      2670 | 2680      2690      2700
                *      *      *      | *      *      *
CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCAAT GCTCACGCTG
                e      e      e PUC19 BACKBONE e      e      e
                                >BsiHKAI
                                |
                                >ApaLI
                                |
                2710      2720      2730 | 2740      2750 | 2760
                *      *      *      | *      *      | *
TAGGTATCTC AGTTCGGTGT AGGTCGTTTC CTCCAAGCTG GGCTGTGTGC ACGAACCCCC
                e      e      e PUC19 BACKBONE e      e      e

```

FIG. 8
(CONTINUED)

35/51

```

      >BsiEI          >BsaWI .
      |              |
      2770          2780          2790          2800          2810          2820
      *            *            *            *            *            *
      CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >AlwNI
      |
      2830          2840          2850          2860          2870          2880
      *            *            *            *            *            *
      ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >SfcI
      |
      2890          2900          2910          2920          2930          2940
      *            *            *            *            *            *
      AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >Eco57I
      |
      2950          2960          2970          2980          2990          3000
      *            *            *            *            *            *
      ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTTG
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      3010          3020          3030          3040          3050          3060
      *            *            *            *            *            *
      ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC AGCAGATTAC
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      3070          3080          3090          3100          3110          3120
      *            *            *            *            *            *
      GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >BspHI
      |
      3130          3140          3150          3160          3170          3180
      *            *            *            *            *            *
      GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCAAAAA GGATCTTCAC
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >DraI          >DraI
      |              |
      3190          3200          3210          3220          3230          3240
      *            *            *            *            *            *
      CTAGATCCTT TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >BamI
      |
      3250          3260          3270          3280          3290          3300
      *            *            *            *            *            *
      TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT
      _____a_____a_____AMP-ORF_____a_____a_____>
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

```

FIG. 8
(CONTINUED)

36/51

```

      >AhdI
      |
      3310      3320      3330      3340      3350      3360
      *      *      *      *      *      *
      TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT
      a      a      AMP-ORF      a      a      >
      e      e      PUC19 BACKBONE      e      e      >

      >BsaI
      |
      >BsrDI      >BpmI      >BsrFI
      |      |      |
      3370      3380      3390      3400      3410      3420
      *      *      *      *      *      *
      ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACC GG CTCCAGATTT
      a      a      AMP-ORF      a      a      >
      e      e      PUC19 BACKBONE      e      e      >

      >BglI
      |
      3430      3440      3450      3460      3470      3480
      *      *      *      *      *      *
      ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC
      a      a      AMP-ORF      a      a      >
      e      e      PUC19 BACKBONE      e      e      >

      >AseI
      |
      3490      3500      3510      3520      3530      3540
      *      *      *      *      *      *
      CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA
      a      a      AMP-ORF      a      a      >
      e      e      PUC19 BACKBONE      e      e      >

      >Psp1406I
      |
      >FspI      >BsrDI      >SfcI      >MslI
      |      |      |      |
      3550      3560      3570      3580      3590      3600
      *      *      *      *      *      *
      TAGTTTGC GC AACGTTGTTG CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTTGG
      a      a      AMP-ORF      a      a      >
      e      e      PUC19 BACKBONE      e      e      >

      >BsaWI
      |
      3610      3620      3630      3640      3650      3660
      *      *      *      *      *      *
      TATGGCTTCA TTCAGTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT
      a      a      AMP-ORF      a      a      >
      e      e      PUC19 BACKBONE      e      e      >

      >BsiEI
      |
      >PvuI      >EaeI
      |      |
      3670      3680      3690      3700      3710      3720
      *      *      *      *      *      *
      GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC
      a      a      AMP-ORF      a      a      >
      e      e      PUC19 BACKBONE      e      e      >

```

FIG. 8
(CONTINUED)

37/51

```

      >MslI
      |
      3730      3740      3750      3760      3770      3780
      *      *      *      *      *      *
      AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT
      _____a_____a_____AMP-ORF_____a_____a_____>
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >ScaI
      |
      3790      3800      3810      3820      3830      3840
      *      *      *      *      *      *
      AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG
      _____a_____a_____AMP-ORF_____a_____a_____>
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >BsiEI
      |
      3850      3860      3870      3880      3890      3900
      *      *      *      *      *      *
      GCGACCGAGT TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGCGCCAC ATAGCAGAAC
      _____a_____a_____AMP-ORF_____a_____a_____>
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >PspI406I
      |
      >DraI      >BsiHKAI      >XmnI
      |      |      |
      3910      3920      3930      3940      3950      3960
      *      *      *      *      *      *
      TTTAAAAGTG CTCATCATTG GAAAACGTTT TTCGGGGCGA AAACCTCTCA GGATCTTACC
      _____a_____a_____AMP-ORF_____a_____a_____>
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >Eco57I
      |
      >ApaLI
      |
      >BssSI      >BsiHKAI
      |      |
      3970      3980      3990      4000      4010      4020
      *      *      *      *      *      *
      GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT
      _____a_____a_____AMP-ORF_____a_____a_____>
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      4030      4040      4050      4060      4070      4080
      *      *      *      *      *      *
      TACTTTCACC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG
      _____a_____a_____AMP-ORF_____a_____a_____>
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

      >MslI      >EarI      >SspI
      |      |      |
      4090      4100      4110      4120      4130      4140
      *      *      *      *      *      *
      AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG
      _____a_____a_____AMP-ORF_____a_____a_____>
      _____e_____e_____PUC19 BACKBONE_____e_____e_____>

```

FIG. 8
(CONTINUED)

38/51

```

                >BspHI   >BsrBI
                |       |
      4150      4160 | 4170      4180      4190      4200
      *         *   *   *         *         *         *
CATTTCATCAG GGTTCATTGTC TCATGAGCGG ATACATATTT GAATGTATTT AGAAAAATAA
_____e_____e_____PUC19 BACKBONE_____e_____e_____>

                                >HincII
                                |
                                >AccI
                                ||
                                >AatII
                                ||
                                >SaiI
                                |||
      4210      4220      4230      4240
      *         *         *         *
ACAAATAGGG GTTCCGCGCA CATTTCCTCCG AAAAGTGCCA CCTGACGTC
_____e_____PUC19 BACKBONE_____e_____>

```

FIG. 8
(CONTINUED)

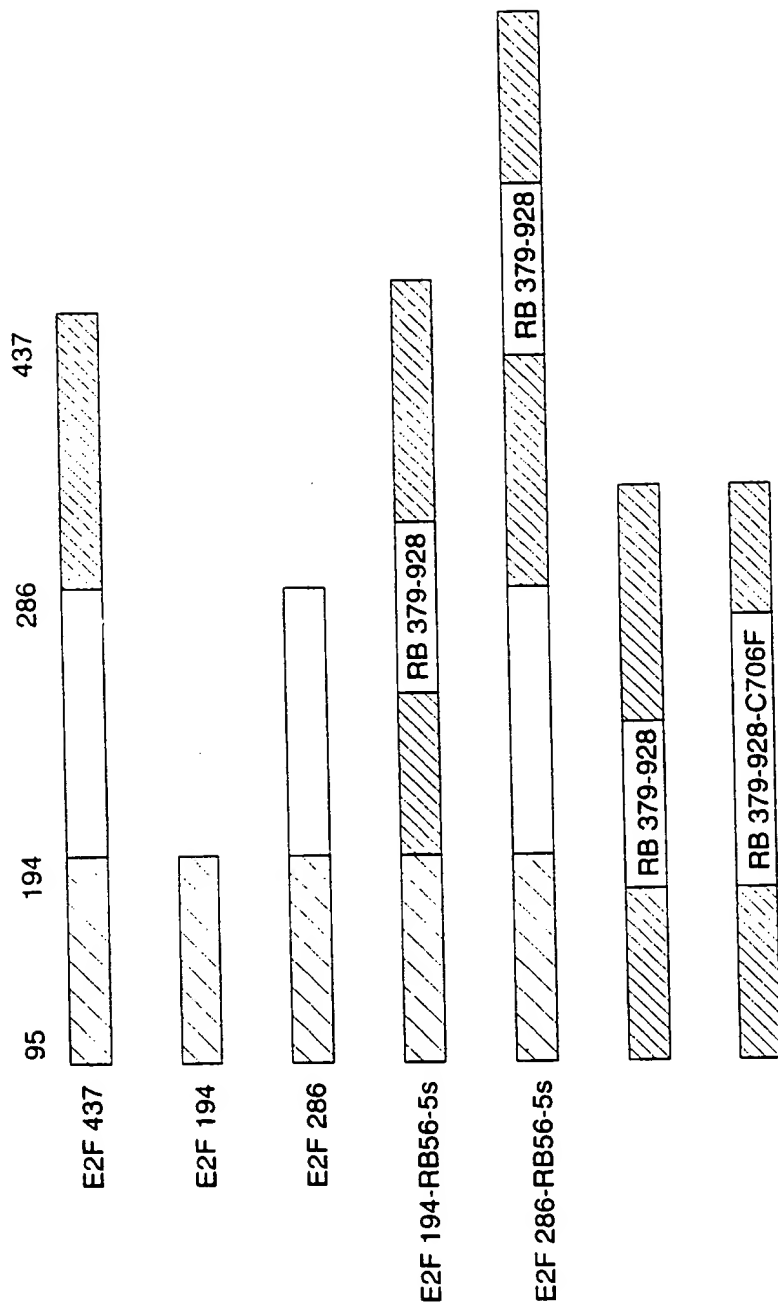


FIG. 9

40/51

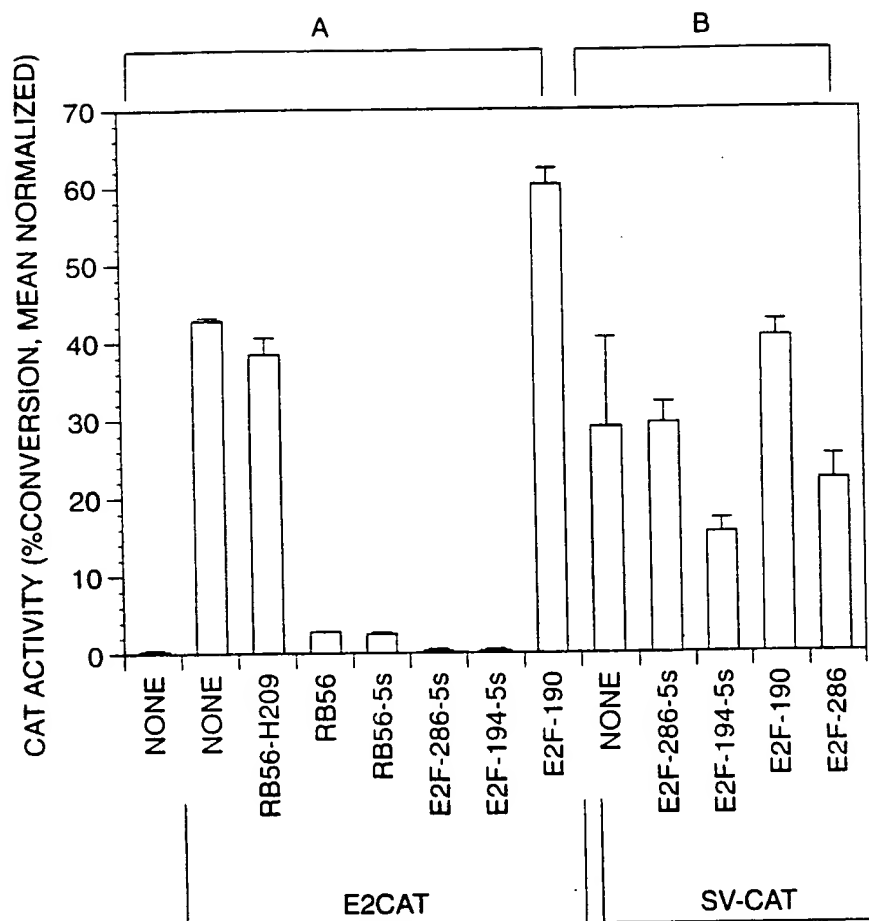
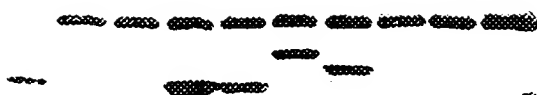


FIG. 10

41/51

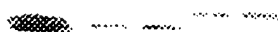
1 2 3 4 5 6 7 8 9 10

FIG. 11A.



1 2 3 4 5

FIG. 11B.



1 2 3 4 5 6 7 8 9

FIG. 11C.



1 2 3 4 5

FIG. 11D.



42/51

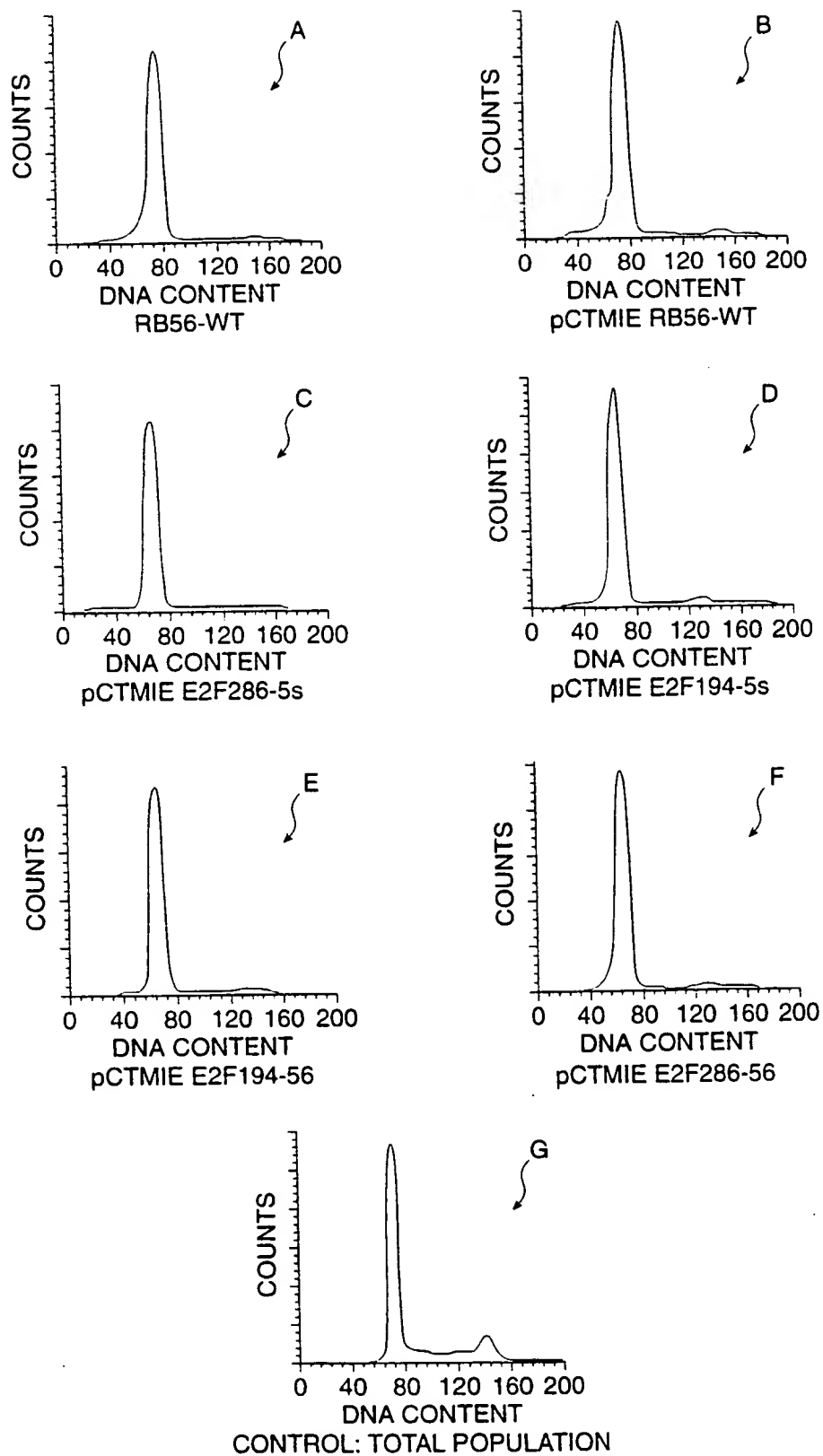


FIG. 12

43/51

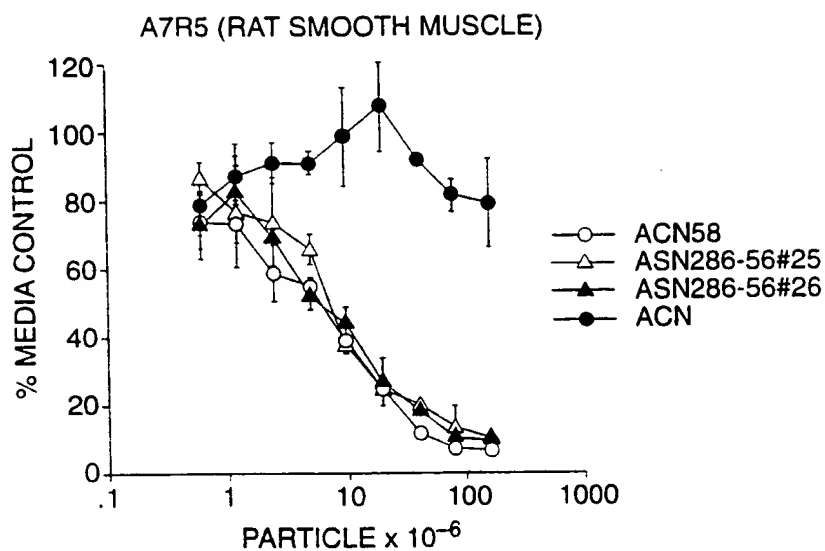


FIG. 13A

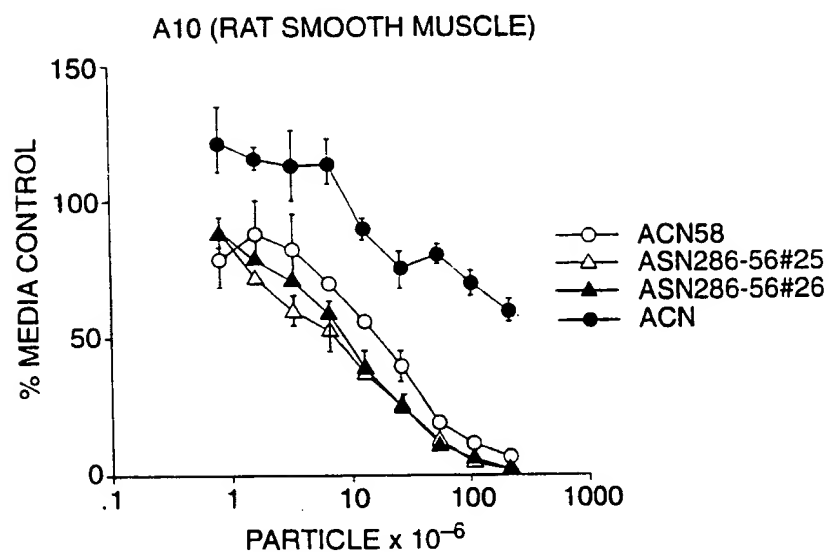


FIG. 13B

44/51

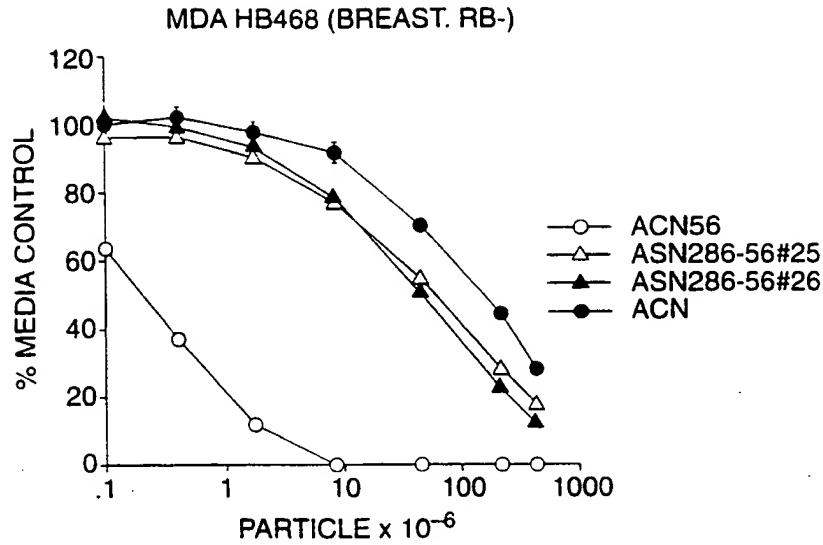


FIG. 14A

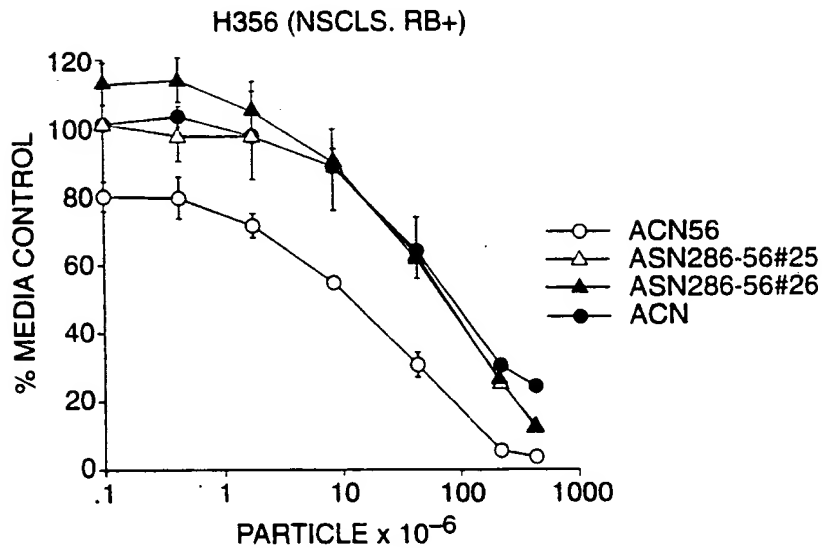
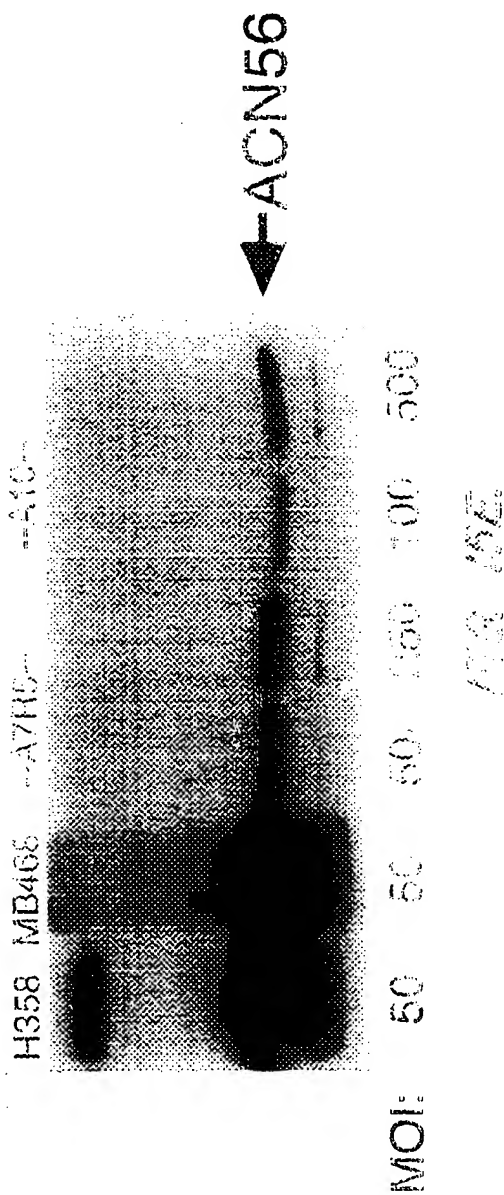


FIG. 14B

45/51

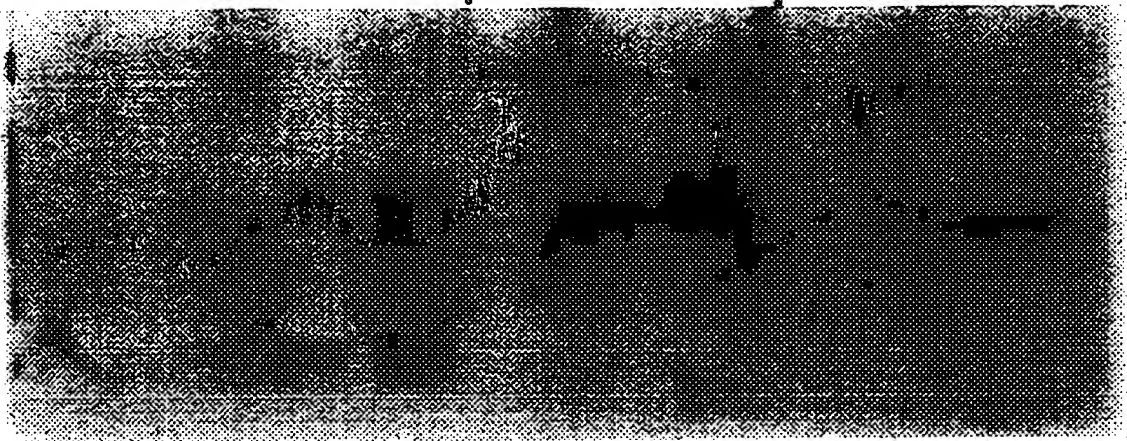


Ad-BGL MOI=5
FIG. 15A. FIG. 15B. FIG. 15C. FIG. 15D.



46/51

MB468 (BREAST) | A7R5 (SM) | A10 (SM)



UM 50 250 500

UM 50 250

UM 100 500

FIG. 16.

47/51

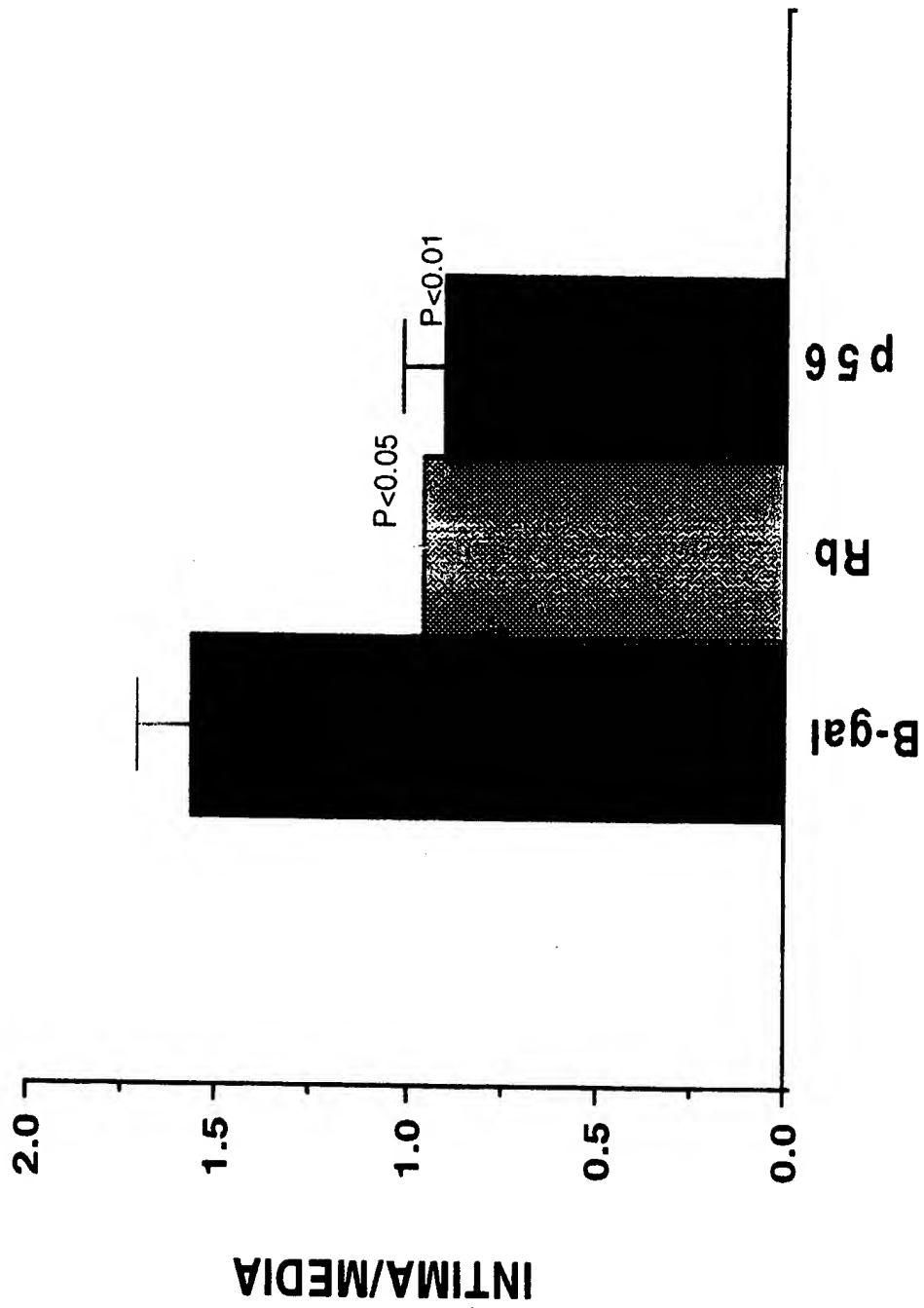
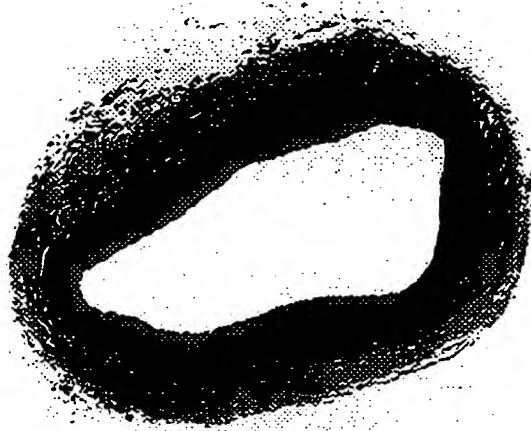


FIG. 17.

48/51



p56^{RB}-Treated



Puromycin



Normal

1998 12

49/51

A7P5 (Muscle)

MOI

MB468 (Breast)

ACNBGAL

ASNBGAL

100 50

FIG 19

50/51

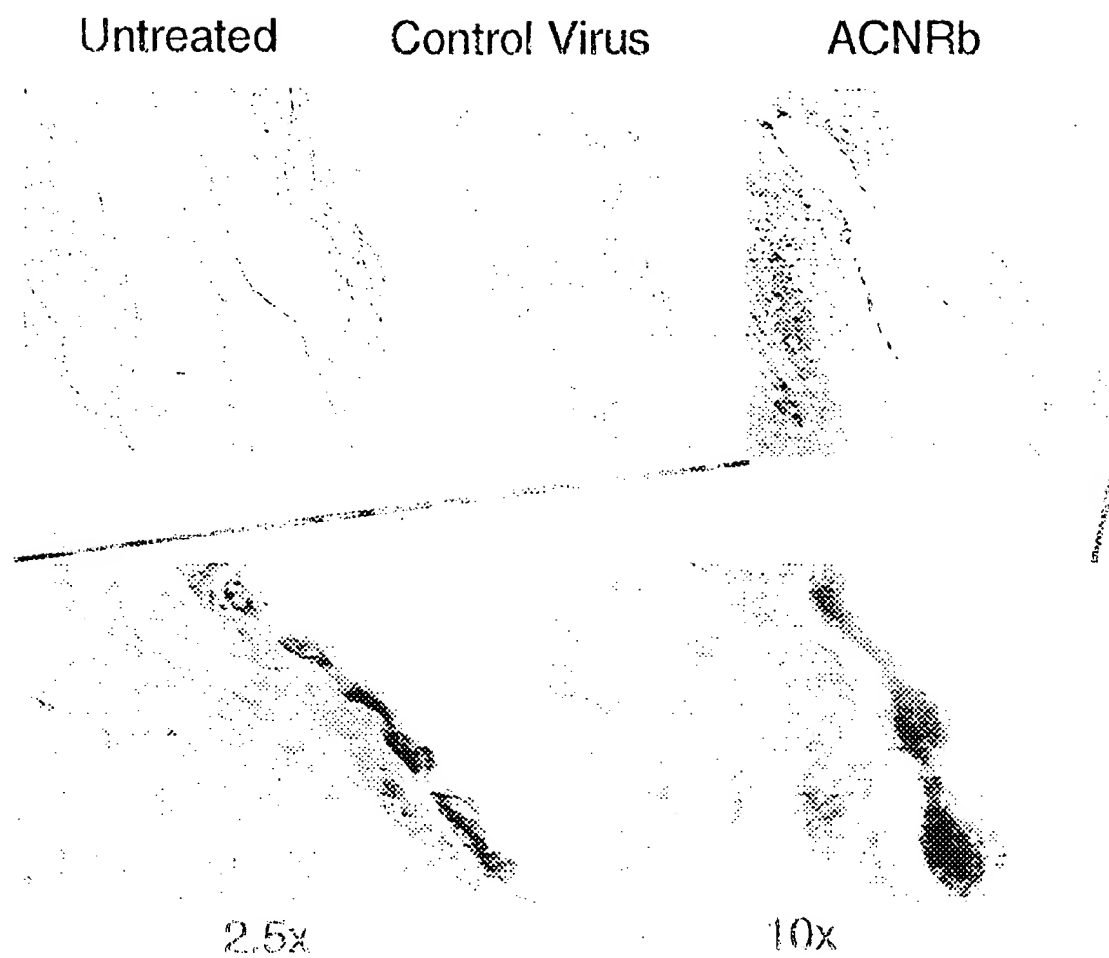


FIG. 20.

51/51

A7r5 3H-THYMIDINE

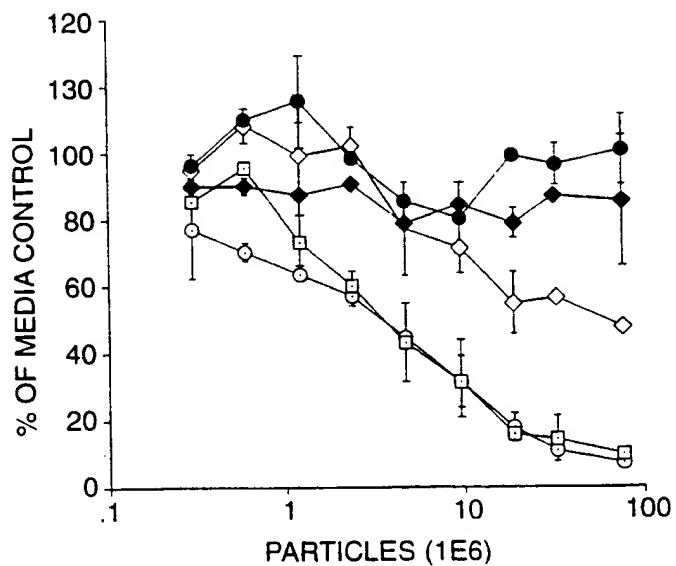


FIG. 21A

MDA468 3H-THYMIDINE

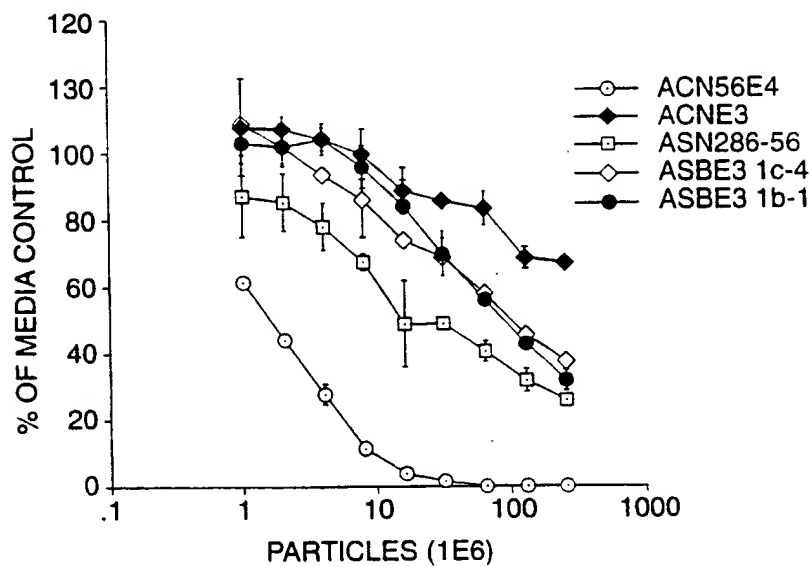


FIG. 21B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/21821**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : C07H 21/04; C07K 5/00; A61K 38/00, 35/12

US CL : 536/23.4, 24.5; 530/300; 424/277.1; 514/2

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.4, 24.5; 530/300; 424/277.1; 514/2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, BIOSIS, SCISEARCH, CANCERLIT, WPIDS, EMBASE

Search terms: retinoblastoma, RB polypeptide, adenovirus vector, transcription factor, restenosis, cancer treatment

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	GOODRICH et al. Administration of a functional retinoblastoma polypeptide or protein-used to prevent and inhibit primary and secondary retinoblastoma linked cancers. WO 9507708 A2. 23 March 1995. Abstract.	1-36
Y	XU et al. Enhanced tumor suppressor gene therapy via replication-deficient adenovirus vectors expressing an N-terminal truncated retinoblastoma protein. Cancer Research. 15 May 1996. Vol.56. No.10. pages 2245-2249, especially abstract.	1-36

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
B earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 18 MARCH 1998	Date of mailing of the international search report 24 APR 1998
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer GEETHA P. BANSAI Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/21821

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	FUEYO et al. Expression of exogenous p16/CDKN2 produces growth arrest in a glioma cell line that does not express Rb protein. Proc. Annual Meeting American Association of Cancer Res. 1996. Vol 37. ppA49. Meeting Abstract.	1-36

Form PCT/ISA/210 (continuation of second sheet)(July 1992)★